

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGWNFSVNGSGSVIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_nhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2409	89.0	516	082839	082839 bacillus sp
2	1942	71.7	533	09A034	Q8aq54 bacillus me
3	1934	71.4	513	081X74	Q8iy74 bacillus an
4	1926	71.1	513	081AS4	Q8las4 bacillus ce
5	1889.5	69.8	613	2 Q59222	Q59222 bacillus sp
6	1874	69.2	519	2 Q9RQ78	Q9rt8 cytophaga s
7	1872.5	69.1	549	2 Q31193	Q31193 bacillus st
8	1867.5	69.0	521	2 P71034	P71034 bacillus sp
9	1867.5	69.0	549	2 Q9KW16	Q9kyw6 bacillus st
10	1813.5	67.0	501	2 Q93148	Q93148 bacillus sp
11	1576.5	58.2	507	16 Q87HG6	Q87hg6 vibrio para
12	1363	50.3	493	2 Q03657	Q03657 bacillus ci
13	1336	49.3	481	16 Q89YF1	Q89yp1 bacteroides
14	1307.5	48.3	486	16 Q8DT08	Q8dt08 streptococc
15	1307.5	48.3	488	16 Q8EOM2	Q8eom2 streptococc
16	1300.5	48.0	488	16 Q8E696	Q8e696 streptococc

17	1298	47.9	484	16	Q97Q49	Q97q49 streptococc
18	1296	47.9	484	16	Q8DFC8	Q8dpc8 streptococc
19	1282	47.3	492	16	Q8YU21	Q8yuz1 anabaena sp
20	1279.5	47.2	486	2	O68875	O68875 streptococc
21	1262.5	46.6	484	2	O50583	O50583 streptococc
22	1260.5	46.5	485	2	Q53786	Q53786 streptococc
23	1148	42.4	491	16	Q9CG59	Q9cg59 lactococcus
24	1114	41.1	506	16	Q8U916	Q8u916 agrobacteri
25	1098	40.5	494	16	Q8Z5S5	Q8z5s5 salmonella
26	1085	40.1	495	16	Q8XBB6	Q8xbb6 escherichia
27	1080	39.9	495	16	Q8FGL8	Q8fgl8 escherichia
28	1073	39.6	495	16	Q7UAB0	Q7uab0 shigella fl
29	1071	39.5	495	16	Q83R40	Q83r40 shigella fl
30	1048.5	38.7	523	3	Q877B1	Q877b1 aspergillus
31	494.5	18.3	461	1	O33476	O33476 pyrococcus
32	494.5	18.3	461	1	Q8NKR4	Q8nkr4 thermococcu
33	475.5	17.6	461	1	Q8NKR5	Q8nkr5 thermococcu
34	467	17.2	469	1	O50200	O50200 thermococcu
35	462.5	17.1	460	1	Q9P9L0	Q9p9l0 pyrococcus
36	462.5	17.1	460	1	O08452	O08452 pyrococcus
37	462.5	17.1	473	17	Q8U3I9	Q8u3i9 pyrococcus
38	459	16.9	432	14	Q8JZK3	Q8jzk3 uncultured
39	444	16.4	457	1	Q93647	Q93647 thermococcu
40	320.5	11.8	482	2	Q60051	Q60051 thermoactin
41	284.5	10.5	421	10	Q7X9T1	Q7x9t1 phaseolus a
42	280	10.3	423	10	Q42678	Q42678 cuscata ref
43	280	10.3	504	1	Q60224	Q60224 natronococc
44	279	10.3	416	10	Q8LJQ6	Q8ljq6 musa acumin
45	278	10.3	424	10	Q8LP27	Q8lp27 pharbitis n

ALIGNMENTS

RESULT 1

082839	PRELIMINARY;	PRT;	516 AA.
ID	082839		
AC	082839;		
DT	01-NOV-1998 (TReMBLrel. 08, Created)		
DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	Amylase.		
OS	Bacillus sp.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1409;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-KSM-1378;		
RX	MEDLINE=98342096; PubMed=9675143;		
RA	Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,		
RA	Ozaki K., Ito S.;		
RT	"Improved thermostability of a Bacillus alpha-amylase by deletion of		
RT	an arginine-glycine residue is caused by enhanced calcium binding."		
RL	Biochem. Biophys. Res. Commun. 248:372-377(1998).		
DR	EMBL; AB008763; BAA32431.1; -		
DR	HSSP; P06278; 1VJS.		
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amyl_cat.		
DR	InterPro; IPR006589; Alp_amyl_cat_sub.		
DR	InterPro; IPR006046; Glyco_hydro_13.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
SO	SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;		

Query Match 89.0%; Score 2409; DB 2; Length 516;

Best Local Similarity 86.0%; Pred. No. 5.9e-143;

Matches 417; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGHNHNRILSDASNLKDKGISAVWIPPAWKGSQNDVGYGA 60

Db 32 HHNGTNGTMQYFEWYLPNDGHNHNRILSDASNLKDKGISAVWIPPAWKGSQNDVGYGA 91

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QY 61. YDLVLDGEFNOKGRTIRTKYGTNRQLOAAVNAKLSNGIQVYGVVNMHKGADATENVRAV 120
DB 62. YDLVLDGEFNOKGRTIRTKYGTNRQLOAAVNAKLSNGIQVYGVVNMHKGADATENVRAV 151
QY 121. EVNPNRNOEVSSEYITIAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
DB 152. EVNPNRNOEVSSEYITIAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 211
QY 181. RGDGKWDWEVDTEGNGYDLYMADIDMDHPEVNVNLRNKGWVYTNLTGLDGFRIDAVKH 240
DB 212. RGTGKAWDWEVDTEGNGYDLYMADIDMDHPEVNVNLRNKGWVYTNLTGLDGFRIDAVKH 271
QY 241. IKYSFTEDWLNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
DB 272. IKYSFTEDWLNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 331
QY 301. SKSGGNYDMROIENGTVQVRHPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTITRE 360
DB 332. SKSGGNYDMROIENGTVQVRHPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTITRE 391
QY 361. QYPSVFYGYGIPGTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 420
DB 392. QYPSVFYGYGIPGTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 451
QY 421. HNSGLATIMSDGAGGNKMFVGRNKAQVWTDITGNRAGTGTVTINADGWNFSVNGSGVS 480
DB 452. HNSGLATIMSDGAGGNKMFVGRNKAQVWTDITGNRAGTGTVTINADGWNFSVNGSGVS 511
QY 481. IWVKQ 485
DB 512. VVVKQ 516

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RESULT 2
Q9AQ54
ID Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
RT KSM B-404."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amil_cat.
DR InterPro; IPR006589; Alp_amil_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

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Query Match 71.7%; Score 1942; DB 2; Length 533;
Best Local Similarity 69.6%; Pred. No. 1.1e-113;
Matches 336; Conservative 57; Mismatches 86; Indels 4; Gaps 2;

QY 6 NGTMMQYFENYLPDNGNHNRLSDASNLKDGISAWIPPAWKGASQNDVGAYDLYD 65
DB 52 NGTMMQYFENYLPDNGNHNRLSDASNLKDGISAWIPPAWKGASQNDVGAYDLYD 111
QY 66 LGSEFNOKGRTIRTKYGTNRQLOAAVNAKLSNGIQVYGVVNMHKGADATENVRAV 125
DB 112 LGSEFNOKGRTIRTKYGTNRQLOAAVNAKLSNGIQVYGVVNMHKGADATENVRAV 171

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QY 126 NNNQVSEYITIAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185
DB 172 NNNQVSEYITIAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 230
QY 186 GHDWEVDTEGNGYDLYMADIDMDHPEVNVNLRNKGWVYTNLTGLDGFRIDAVKH 245
DB 231 AMDWEVSENGYDLYMADIDMDHPEVNVNLRNKGWVYTNLTGLDGFRIDAVKH 290
QY 246 TRDMLNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLYNAKSGG 305
DB 291 LEDWVNHVSATGKMFVAEFAWFKNDLGAENYLNKTNWNSVDFVPLHYNLYNAKSGG 350
QY 306 NYDMRQIENGTVQVRHPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTITRE 365
DB 351 NYDMRQIENGTVQVRHPHVAITFVDNHDSPQEEALESFVEWFKPLAYALTITRE 410
QY 366 VYGYGYGIPGTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 422
DB 411 VYGYGYGIPGTHGVPMKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 470
QY 423 NSGLATIMSDGAGGNKMFVGRNKAQVWTDITGNRAGTGTVTINADGWNFSVNGSGVS 482
DB 471 NSGLATIMSDGAGGNKMFVGRNKAQVWTDITGNRAGTGTVTINADGWNFSVNGSGVS 530
QY 483 VNK 485
DB 531 VQR 533

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RESULT 3
Q81YJ4
ID Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nietman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koshler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AB017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amil_cat.
DR InterPro; IPR006589; Alp_amil_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

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Query Match 71.4%; Score 1934; DB 16; Length 513;
Best Local Similarity 69.4%; Pred. No. 3.4e-113;
Matches 335; Conservative 59; Mismatches 85; Indels 4; Gaps 2;

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTNGTMMQYFEWILPND.....ADGHWGNSVGGSVVWVKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2613	96.3	516	2	O82839
2	1962	72.3	513	16	Q81YJ4 bacillus sp
3	1956	72.1	533	16	Q81A54
4	1956	72.1	533	2	Q9AQS4
5	1947.5	71.8	613	2	Q59222 bacillus sp
6	1918	70.7	519	2	Q9QRT8 cytophaga s
7	1907.5	70.3	549	2	Q31193 bacillus st
8	1902.5	70.1	521	2	P71034
9	1902.5	70.1	549	2	Q9KMY6 bacillus sp
10	1835.5	67.6	501	2	Q93148 bacillus sp
11	1544.5	56.9	507	16	Q87H66 vibrio para
12	1344	49.5	493	2	Q03657 bacillus ci
13	1329	49.0	481	16	Q89YPI bacteroides
14	1274.5	47.0	486	16	Q8DT08 streptococc
15	1259.5	46.4	488	16	Q8EOM2 streptococc
16	1256.5	46.3	488	16	Q8E696 streptococc

17	1245	45.9	484	16	Q97Q49
18	1243	45.8	484	16	Q8DPC8 streptococc
19	1239	45.7	492	16	Q8YU21
20	1235.5	45.5	486	2	O68875 streptococc
21	1233.5	45.1	484	2	O50583 streptococc
22	1205.5	44.4	485	2	Q53786 streptococc
23	1127	41.5	491	16	Q9CG59 lactococcu
24	1097	40.4	506	16	Q8U916
25	1066	39.3	494	16	Q8Z5S5 salmonella
26	1054	38.8	495	16	Q8XBB6 escherichia
27	1054	38.8	495	16	Q8FGL8 escherichia
28	1047	38.6	495	16	Q7UAB0 shigella fl
29	1045	38.5	495	16	Q83R40 shigella fl
30	1011.5	37.3	529	3	Q877B1 aspergillus
31	475.5	17.5	461	1	Q8NKR4 thermococcu
32	473.5	17.4	461	1	O33476 pyrococcus
33	470	17.3	469	1	O50200 thermococcu
34	469.5	17.3	460	1	Q9P910 pyrococcus
35	469.5	17.3	460	1	O08452 pyrococcus
36	469.5	17.3	473	17	Q8U319 pyrococcus
37	460	16.9	461	1	Q8NKR5 thermococcu
38	451	16.6	432	14	Q8JZK3 uncultured
39	447	16.5	457	1	O93647 thermococcu
40	303	11.2	416	10	Q8LJQ6 musa acumin
41	303	11.2	424	10	Q8LP27 pharbitis n
42	300.5	11.1	421	10	Q7X9T1 phaseolus a
43	298	11.0	420	10	Q9ZP43 phaseolus v
44	295.5	10.9	482	2	Q60051 thermoactin
45	292	10.8	416	10	Q8GUR0 musa acumin

ALIGNMENTS

RESULT 1

O82839 ID O82839 PRELIMINARY; PRT; 516 AA.
AC O82839;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
ON NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RX MEDLINE=98342096; PubMed=9675143;
RA Igarashi K., Hatada Y., Ikawa K., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding.";
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL; AB008763; BAA32431.1; -;
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco hydro_l3.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match Best Local Similarity 96.3%; Score 2613; DB 2; Length 516;

Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWILPNDGHNHNRLLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60

Db 32 HHNGTNGTMMQYFEWILPNDGHNHNRLLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 91

QY 61 YDLYLDFEFGNKGTVRTKYGTGRNOLQAAVTSKNGKIQVYGDVVMNHKGADGTEIYNAV 120
 DB 92 YDLYLDFEFGNKGTVRTKYGTGRNOLQAAVTSKNGKIQVYGDVVMNHKGADGTEIYNAV 151
 QY 121 EVNRSNRNQTSGEYAIATWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180
 DB 152 EVNRSNRNQTSGEYAIATWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 211
 QY 181 RGTGKAWDEWDTENGNDYLYMYADVDMDHPEVTHELRNMGVWYTNLNLGDFRIDAVKH 240
 DB 212 RGTGKAWDEWDTENGNDYLYMYADVDMDHPEVTHELRNMGVWYTNLNLGDFRIDAVKH 271
 QY 241 IKYFTTRDLWTHVRNTTGKPMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNA 300
 DB 272 IKYFTTRDLWTHVRNTTGKPMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNA 331
 QY 301 SNSGGYIDMRNLINGSVQKHPTTHAVTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE 360
 DB 332 SNSGGYIDMRNLINGSVQKHPTTHAVTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE 391
 QY 361 QGYPSVFYGDYIGTPHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNS 420
 DB 392 QGYPSVFYGDYIGTPHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNS 451
 QY 421 HPNSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTGTINADGWGNSVNSGVS 480
 DB 452 HPNSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTGTINADGWGNSVNSGVS 511
 QY 481 VVVKQ 485
 DB 512 VVVKQ 516

RESULT 2

Q81YJ4 ID Q81YJ4 PRELIMINARY; PRT; 513 AA.
 AC Q81YJ4;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Alpha-amylose.
 GN AMYS OR BA3551.
 OS Bacillus anthracis (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=198094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608414; PubMed=12721629;
 RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkak L.M., Gwinn M.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
 RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
 RA Fraser C.M.;
 RT "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria."
 RL Nature 423:81-86(2003).
 DR EMBL; AE017035; AAP27311.1; --
 DR TIGR; BA3551;
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_aml cat.
 DR InterPro; IPR006589; Alp_aml cat_sub.
 DR Pfam; PF00128; alpha-amylose; 1.
 DR SMART; SM00642; Amy; 1.
 DR Complete proteome.
 DR NCBI; 513 AA; 58445 MW; 558D6EF282FD159B CRC64;
 SEQUENCE

Query Match 72.3%; Score 1962; DB 16; Length 513;
 Best Local Similarity 70.2%; Pred. No. 5.6e-119;
 Matches 339; Conservative 63; Mismatches 77; Indels 4; Gaps 2;
 QY 6 NGTMMQYFEMYLFPDNGNHNRLRDDAANLKSXGTAIVWIPPAWKGTSONDVGAYDLYD 65
 DB 32 NGTMMQYFEMYLFPDNGNHNRLRDDAANLKSXGTAIVWIPPAWKGTSONDVGAYDLYD 91
 QY 66 LGFENQKGTVRKYGTGRNOLQAAVTSKNGKIQVYGDVVMNHKGADGTEIYNAV 125
 DB 92 LGFENQKGTVRKYGTGRNOLQAAVTSKNGKIQVYGDVVMNHKGADGTEIYNAV 151
 QY 126 NRNQTSGEYAIATWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKRGCTOK 185
 DB 152 NRNQTSGEYAIATWTKFDFPGGRNNHSSFKRWYHFDGTDWDQSRQLQNKIYKRGCTOK 210
 QY 186 AWDNEVDTEGNDYLYMYADVDMDHPEVTHELRNMGVWYTNLNLGDFRIDAVKH 245
 DB 211 AWDNEVDTEGNDYLYMYADVDMDHPEVTHELRNMGVWYTNLNLGDFRIDAVKH 270
 QY 246 TRDMLTHVRNTTGKPMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNASNSGG 305
 DB 271 TRDMLTHVRNTTGKPMFAVAEFKNDLGALENLYNKTNNHSHVDFVPLHYNLYNASNSGG 330
 QY 306 YDMRNILINGSVQKHPTTHAVTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE 365
 DB 331 YDMRNILINGSVQKHPTTHAVTFVDNHDSPQGEALSFVQOWFKPLAYALVLTRE 390
 QY 366 VFYGDYIGTPHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNSHP 422
 DB 391 VFYGDYIGTPHGVPAKMSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTRGNSHP 450
 QY 423 NSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTGTINADGWGNSVNSGVS 482
 DB 451 NSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTGTINADGWGNSVNSGVS 510
 QY 483 VKQ 485
 DB 511 VKQ 513
 RESULT 3
 Q81AS4 ID Q81AS4 PRELIMINARY; PRT; 513 AA.
 AC Q81AS4;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Glucan 1,4-alpha-maltonhexaoidase (EC 3.2.1.98).
 GN BC3482.
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis."
 RL Nature 423:87-91(2003).
 DR EMBL; AE017009; AAP10417.1; --
 DR GO; GO:0004556; F:alpha-amylose activity; IEA.
 DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_aml cat.
 DR InterPro; IPR006589; Alp_aml cat_sub.
 DR Pfam; PF00128; alpha-amylose; 1.
 DR SMART; SM00642; Amy; 1.
 DR Complete proteome.
 DR NCBI; 513 AA; 58445 MW; 558D6EF282FD159B CRC64;
 SEQUENCE

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGWNFSVNGSVVWKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2613	96.3	516	2	O82839
2	1962	72.3	513	16	O81YJ4
3	1956	72.1	513	16	O81AS4
4	1956	72.1	533	2	O9A054
5	1947.5	71.8	613	2	O59222
6	1918	70.7	519	2	O9ROT8
7	1907.5	70.3	549	2	O31193
8	1902.5	70.1	521	2	P71034
9	1902.5	70.1	549	2	O9KWY6
10	1835.5	67.6	501	2	O93148
11	1544.5	56.9	507	16	O87HG6
12	1344	49.5	493	2	O03657
13	1329	49.0	481	16	O89YI1
14	1274.5	47.0	486	16	O8DT08
15	1259.5	46.4	488	16	O8E0M2
16	1256.5	46.3	488	16	O8E696

ALIGNMENTS

RESULT 1

O82839 ID O82839 PRELIMINARY; PRT; 516 AA.
AC O82839.

BT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RX MEDLINE=98342096; PubMed=9675143;
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL; AB008763; BAA32431.1; -;
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Glyco_hydro_13.
DR PRINTS; PR00128; alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 516 AA; 5841 MW; D90A8C90ECC182F8 CRC64;

Query Match 96.3%; Score 2613; DB 2; Length 516;
Best Local Similarity 95.1%; Pred. No. 4.1e-161;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGHNHNRLLDDAANLKSIGITAVWIPPAWKGTSDNDVGYGA 60
Db 32 HHNGTGTMMQYFEWYLPNDGHNHNRLLDDAANLKSIGITAVWIPPAWKGTSDNDVGYGA 91

Q97Q49 streptococ
Q8DPC8 streptococ
Q8YU21 anabaena sp
Q68875 streptococ
Q50583 streptococ
Q53786 streptococ
Q9C959 lactococcus
Q8U916 agrobacteri
Q82585 salmonella
Q8XBB6 escherichia
Q8FGL8 escherichia
Q7UAB0 shigella fl
Q83F40 shigella fl
Q877B1 aspergillus
Q8NKR4 thermococcu
Q33476 pyrococcus
Q50200 thermococcu
Q9P910 pyrococcus
Q08452 pyrococcus
Q8U319 pyrococcus
Q8NKR5 thermococcu
Q8JZK3 uncultured
Q53647 thermococcu
Q81Q66 musa acumin
Q81P27 pharbitis n
Q7X9T1 phaseolus a
Q92P43 phaseolus v
Q60051 thermoactin
Q8GUR0 musa acumin

KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BFF9F6 CRC64;

Query Match 72.1%; Score 1956; DB 16; Length 513;
Best Local Similarity 70.4%; Pred. No. 1.4e-118;
Matches 340; Conservative 58; Mismatches 81; Indels 4; Gaps 2;

QY 6 NGTMQYFEWYLPNDGNHNRRLDAAANLKSIGITAVIIPPAWKTSQNDVGYGAYDLYD 65
DB 32 NGTLMQYFEWYLPNDGNHNRRLDVENLAEGKITSVMIPPAKGTQNDVGYGAYDLYD 91
QY 66 LGFENQKGTVRTKGTGRNQLQAAVTSLKNGIQVYGDVVMNHKGGADTETVNAVEVNR 125
DB 92 LGFENQKGTVRTKGTGRNQLQAAVTSLKNGIQVYGDVVMNHKGGADTETVNAVEVNR 151
QY 126 NRNETSGEVAIEAWTKPDPGRGNHSSFKRWYHFDGTDWDSROLQNKIYKFRGTGK 185
DB 92 LGFENQKGTVRTKGTGRNQLQAAVTSLKNGIQVYGDVVMNHKGGADTETVNAVEVNR 151
QY 126 NRNETSGEVAIEAWTKPDPGRGNHSSFKRWYHFDGTDWDSROLQNKIYKFRGTGK 185
DB 152 NRNEVSGDYEISAWTGFNPGRGDSYFNFKWYHFDGTDWDSGRKL-NRIYKFRGTGK 210
QY 186 AWDHEVDTEGNNGYDLYMAYADVDMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHISYF 245
DB 211 AWDHEVSENGNYDLYMAYADLDLDPDPAVEMKMGWYANLNLGDFRLDAVXHDHEY 270
QY 246 TRDLWTHVRNTTKPMFAVAEFAWKNLGAENYLNKTSWHSVDFDPLHYNLNASGG 305
DB 271 LRDMVNHVRQQTGKEMFTVAEYQNDIQTLNNYLAKVYNSQSFDAFLHYNFHYASTGNG 330
QY 306 YYDMRNILNSVQKHPHTAVTFVDNHDSPGAELESFVQOQFPLAYALVLTREOGYPS 365
DB 331 NYDMRNILKGTVANHPHTAVTLVENHDSQPQSLESVSPWPKFLAYAFILTRAEGYPS 390
QY 366 VFYGDYXGI---PTHGVPAKMSKIDPLLOARQTFAYGTQHDYDFDHHDIIGWTRGNSHP 422
DB 391 VFYGDYXGKNSNYEIPALKDKIDPILTARKNFAYGTQRDYDFDHPDVGWTRGDSVHA 450
QY 423 NSGLATIMSDPGGNKMYGVGNKAGQWRDITGNRTGTVTINADGNFVNGSGSVW 482
DB 451 NSGLATLISDGPAGKMWGVGNKAGEIWDITGNQNTVTINKDQGWQFQVSGSVSIY 510
QY 483 VKQ 485
DB 511 VQ 513

RESULT 4
Q9AQ54
ID Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha-amyase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT KSM B-404.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSP; P06278; IYVS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR Pfam; PF00128; alpha-amyase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 72.1%; Score 1956; DB 2; Length 533;

Best Local Similarity 70.2%; Pred. No. 1.4e-118;
Matches 339; Conservative 61; Mismatches 79; Indels 4; Gaps 2;

QY 6 NGTMQYFEWYLPNDGNHNRRLDAAANLKSIGITAVIIPPAWKTSQNDVGYGAYDLYD 65
DB 52 NGTLMQYFEWYLPNDGNHNRRLDVENLAEGKITSVMIPPAKGTQNDVGYGAYDLYD 111
QY 66 LGFENQKGTVRTKGTGRNQLQAAVTSLKNGIQVYGDVVMNHKGGADTETVNAVEVNR 125
DB 112 LGFENQKGTVRTKGTGRNQLQAAVTSLKNGIQVYGDVVMNHKGGADTETVNAVEVNR 171
QY 126 NRNETSGEVAIEAWTKPDPGRGNHSSFKRWYHFDGTDWDSROLQNKIYKFRGTGK 185
DB 172 NRNEVSGDYEISAWTGFNPGRGDSYFNFKWYHFDGTDWDSGRKL-NRIYKFRGTGK 230
QY 186 AWDHEVDTEGNNGYDLYMAYADVDMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHISYF 245
DB 231 AWDHEVSENGNYDLYMAYADLDLDPDPAVEMKMGWYANLNLGDFRLDAVXHDHEY 290
QY 246 TRDLWTHVRNTTKPMFAVAEFAWKNLGAENYLNKTSWHSVDFDPLHYNLNASGG 305
DB 291 LRDMVNHVRQQTGKEMFTVAEYQNDIQTLNNYLAKVYNSQSFDAFLHYNFHYASTGNG 350
QY 306 YYDMRNILNSVQKHPHTAVTFVDNHDSPGAELESFVQOQFPLAYALVLTREOGYPS 365
DB 351 NYDMRNILKGTVANHPHTAVTLVENHDSQPQSLESVSPWPKFLAYAFILTRAEGYPS 410
QY 366 VFYGDYXGI---PTHGVPAKMSKIDPLLOARQTFAYGTQHDYDFDHHDIIGWTRGNSHP 422
DB 411 VFYGDYXGKNSNYEIPALKDKIDPILTARKNFAYGTQRDYDFDHPDVGWTRGDSVHA 470
QY 423 NSGLATIMSDPGGNKMYGVGNKAGQWRDITGNRTGTVTINADGNFVNGSGSVW 482
DB 471 NSGLATLISDGPAGKMWGVGNKAGEIWDITGNQNTVTINKDQGWQFQVSGSVSIY 530
QY 483 VKQ 485
DB 531 VQ 533

RESULT 5
Q59222
ID Q59222 PRELIMINARY; PRT; 613 AA.
AC Q59222
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha-amyase (EC 3.2.2.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin L.-L., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22045; AAA63900.1; -.
DR HSP; P06278; IYVS.
DR GO; GO:0004556; F:alpha-amyase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat_sub.
DR InterPro; IPR002044; CBD 4.
DR Pfam; PF00128; alpha-amyase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD 4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.

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SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
Query Match 71.8%; Score 1947.5; DB 2; Length 613;
Best Local Similarity 70.3%; Pred. No. 6.1e-118; Indels 1; Gaps 1;
Matches 336; Conservative 66; Mismatches 75;

QY 6 NGTMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSONDVGAYDLYD 65
DB 36 NETMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSONDVGAYDLYD 95

QY 66 LGFENOKGTVRTKYGTRNQLAAVTSLNKNGIOYQYGVVNMHKGAGDGTETVNAVEVNR 125
DB 96 LGFENOKGTVRTKYGTRNQLAAVTSLNKNGIOYQYGVVNMHKGAGDGTETVNAVEVNR 155

QY 126 NNRQETSGEYAIKAWTKFDPFGRGNHSSFKRWYHFDGTDQSDQSLQNKIKYKFRGTGK 185
DB 156 NNRQETSGETYQIAWTKFDPFGRGNHSSFKRWYHFDGTDQSDQSLQNKIKYKFRGTGK 214

QY 186 AWDWEVDTEGNYDYLMDYADVDMDHPEVIHELNRNGVWYTNLTNLGDGFRIDAVKHIKYSF 245
DB 215 AWDWEVDTEGNYDYLMDYADVDMDHPEVIHELNRNGVWYTNLTNLGDGFRIDAVKHIKYSF 274

QY 246 TRDMLTHVRNTTKGPMFAVAFKWDNLGAIENYLNKTSWNHSDVPDPLHNLNANSNG 305
DB 275 FPDWLTIVRNQTKNLFVAGFWSYDVKNLHNTITKNGSMFLDAPLHNNFYTASKSSG 334

QY 306 YDWMENILNGSVQKHPTAVTFVDNHDSDQGEALSFVQWFKPLAYALVLTREGQYPS 365
DB 335 YFDMRYLLNLTWKDQSLAVTLVDNHDTPQGSLSWFEWFKPLAYAFILTRQSGYPC 394

QY 366 VFYGDYGGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHHDIIIGWTREGNSHPNSG 425
DB 395 VFYGDYGGIPKYNIPGLKSKIDPLLIARDYAYGTQHDYFDHHDIIIGWTREGIDTKPNSG 454

QY 426 LATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGVTINADGWNFSGVSGSVWV 483
DB 455 LAALITDGGGSKMWYGVKKHAGKFYDILTGNRSDTVTINADGWBKFGKNGSGSVISWV 512

RESULT 6
ID Q9RQ78 PRELIMINARY; PRT; 519 AA.
AC Q9RQ78
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF00567.1; -.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 519 AA; 58337 MW; 3B6B88A4DF98B163 CRC64;
Query Match 70.7%; Score 1918; DB 2; Length 519;
Best Local Similarity 69.2%; Pred. No. 4e-116; Indels 4; Gaps 2;
Matches 335; Conservative 67; Mismatches 78;

SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;
Query Match 70.3%; Score 1907.5; DB 2; Length 549;
Best Local Similarity 68.6%; Pred. No. 2.1e-115; Indels 1; Gaps 1;
Matches 328; Conservative 70; Mismatches 79;

QY 6 NGTMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSONDVGAYDLYD 65
```

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QY 5 TNGTMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSONDVGAYDLYD 64
DB 37 TNGTMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSONDVGAYDLYD 96

QY 65 DLGEFNOKGTVRTKYGTRNQLAAVTSLNKNGIOYQYGVVNMHKGAGDGTETVNAVEVNR 124
DB 97 DLGEFNOKGTVRTKYGTRNQLAAVTSLNKNGIOYQYGVVNMHKGAGDGTETVNAVEVNR 156

QY 125 SNRNQETSGEYAIKAWTKFDPFGRGNHSSFKRWYHFDGTDQSDQSLQNKIKYKFRGTG 184
DB 157 SNRNQETSSEYNIQAWTGFFGRGTTYSNFKWQHFHFDGTDQSDQSLQNKIKYKFRGTG 215

QY 185 KAWDWEVDTEGNYDYLMDYADVDMDHPEVIHELNRNGVWYTNLTNLGDGFRIDAVKHIKYS 244
DB 216 KAWDWEVSENGNYDYLMDYADVDMDHPEVIHELNRNGVWYTNLTNLGDGFRIDAVKHIKYS 275

QY 245 FTRDMLTHVRNTTKGPMFAVAFKWDNLGAIENYLNKTSWNHSDVPDPLHNLNANSNG 304
DB 276 FLKDWYDNRATATGEMFTVGEYQNDLGALNNYLAKVNYNQSLFDAPLHNFYAASTGG 335

QY 305 GYDWMENILNGSVQKHPTAVTFVDNHDSDQGEALSFVQWFKPLAYALVLTREGQYPS 364
DB 336 GYDWMENILNTIVASNPATKAVTLVENHDTQGSLESTVQWFKPLAYAFILTRSGGYP 395

QY 365 SVFYGDYGGIPTHGVPAKMSKIDPLLOARQTFAYGTQHDYFDHHDIIIGWTREGNSSH 421
DB 396 SVFYGDYMGTKGTTREIPALKSKIEPLKARKDQVAYGTQHDYFDHHDIIIGWTREGDSTK 455

QY 422 PMSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGVTINADGWNFSGVSGSV 481
DB 456 AKSGLATVITDGGGSKRMVGTSGNAGEIWDLTGNRTDKITIGSDGYATFPVNGGVS 515

QY 482 WVKQ 485
DB 516 WVKQ 519

RESULT 7
ID Q31193 PRELIMINARY; PRT; 549 AA.
AC Q31193
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha amylase.
GN AMI.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF032864; AAB86961.1; -.
DR PIR; A54541; A54541.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;
Query Match 70.3%; Score 1907.5; DB 2; Length 549;
Best Local Similarity 68.6%; Pred. No. 2.1e-115; Indels 1; Gaps 1;
Matches 328; Conservative 70; Mismatches 79;

QY 6 NGTMMQYFEWYLPNDGNHNRDLDDAANLKSKGITAVWIPPAWKGTSONDVGAYDLYD 65
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|||||
39 NGTMMQYFEWYLPDDGTLTKVANEANLSSGLTALWLPAYKGTSRSDVGYGYDLYD 98
66 LGFENQKGTVRTKYGTRNQLQAAVTSLKNGIQYQYGVDMVNMHKGADGTEIVNAVEVNR 125
99 LGFENQKGTVRTKYGTRKQYLAQIAAAHAAGMAYADVDFHKGADGTEWDAVEVNP 158
126 NRQNETSGEYAEIAEWTKFDPGRGNHSSFKRWYHFDGTDQDOSROLQNKIYKFRGTGK 185
159 DRNQEISGTQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
186 AWDWEVDTENGNDYLMYADVDMHPEVTHELRNWGVYNTNLDGFRIDAVKHKYSF 245
218 AWDWEVDTENGNDYLMYADLMDHPEVTVLKNWGWYNTNIDGFRDLDAVKHKEFSF 277
246 TRDWLTHVRNTGKPMFAVAFWKNLDGAIENYLNKTSWNHSDVPDLPHNLNNAASGG 305
278 FPDWLSVRSQTGKPLFTVGEYMSYDINKLHNYITKTNGTMSLFDAPLHNFYTASKSGG 337
306 YYDMRNILNGSVVQKHPHTHATVFDVNDHSDQGEALSFVQOWFKPLAYALVLTREOGYPS 365
338 AFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEGYPC 397
366 VFYGDYGIPTGHPVPMKSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTREGNSHPNSG 425
398 VFYGDYGIPTGHPVPMKSKIDPLLIARRDYAYGTQHDYLDHSDIIIGWTREGVTEKPGSG 457
426 LATIMSDPGCGNKMVYGVKNGKAGQWRDITGNRTGTVTINADGWNFSVNGGVSVMV 483
458 LAALITDGPCKGKMWYGVKGQHAGKVFYDLTGNSRSDTVTINSDGWFGEFKVNGGVSVMV 515

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RESULT 8

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P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC P71034;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=541116;
RN [1]
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
the most stable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005375; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

```

Query Match 70.1%; Score 1902.5; DB 2; Length 521;
 Best Local Similarity 68.4%; Pred. No. 4.1e-115;
 Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;

```

6 NGTMMQYFEWYLPDDGTLTKVANEANLSSGLTALWLPAYKGTSRSDVGYGYDLYD 65
39 NGTMMQYFEWYLPDDGTLTKVANEANLSSGLTALWLPAYKGTSRSDVGYGYDLYD 98

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66 LGFENQKGTVRTKYGTRNQLQAAVTSLKNGIQYQYGVDMVNMHKGADGTEIVNAVEVNR 125
99 LGFENQKGTVRTKYGTRKQYLAQIAAAHAAGMAYADVDFHKGADGTEWDAVEVNP 158
126 NRQNETSGEYAEIAEWTKFDPGRGNHSSFKRWYHFDGTDQDOSROLQNKIYKFRGTGK 185
159 DRNQEISGTQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
186 AWDWEVDTENGNDYLMYADVDMHPEVTHELRNWGVYNTNLDGFRIDAVKHKYSF 245
218 AWDWEVDTENGNDYLMYADLMDHPEVTVLKNWGWYNTNIDGFRDLDAVKHKEFSF 277
246 TRDWLTHVRNTGKPMFAVAFWKNLDGAIENYLNKTSWNHSDVPDLPHNLNNAASGG 305
278 FPDWLSVRSQTGKPLFTVGEYMSYDINKLHNYITKTNGTMSLFDAPLHNFYTASKSGG 337
306 YYDMRNILNGSVVQKHPHTHATVFDVNDHSDQGEALSFVQOWFKPLAYALVLTREOGYPS 365
338 AFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEGYPC 397
366 VFYGDYGIPTGHPVPMKSKIDPLLOAROTFAYGTQHDYFDHHDIIIGWTREGNSHPNSG 425
398 VFYGDYGIPTGHPVPMKSKIDPLLIARRDYAYGTQHDYLDHSDIIIGWTREGVTEKPGSG 457
426 LATIMSDPGCGNKMVYGVKNGKAGQWRDITGNRTGTVTINADGWNFSVNGGVSVMV 483
458 LAALITDGPCKGKMWYGVKGQHAGKVFYDLTGNSRSDTVTINSDGWFGEFKVNGGVSVMV 515

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RESULT 9

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Q9KMY6
ID Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC Q9KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRC64;

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Query Match 70.1%; Score 1902.5; DB 2; Length 549;
 Best Local Similarity 68.4%; Pred. No. 4.3e-115;
 Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;

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6 NGTMMQYFEWYLPDDGTLTKVANEANLSSGLTALWLPAYKGTSRSDVGYGYDLYD 65
39 NGTMMQYFEWYLPDDGTLTKVANEANLSSGLTALWLPAYKGTSRSDVGYGYDLYD 98

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66 LGFENQKGTVRTKYGTRNQLQAAVTSLKNGIQYQYGVDMVNMHKGADGTEIVNAVEVNR 125
99 LGFENQKGTVRTKYGTRKQYLAQIAAAHAAGMAYADVDFHKGADGTEWDAVEVNP 158
126 NRQNETSGEYAEIAEWTKFDPGRGNHSSFKRWYHFDGTDQDOSROLQNKIYKFRGTGK 185

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```
Db 322 SGGYDMRQIMNGITLMKDNPNKAVTLVENHDTQPLQALESTVDMWFKPLAFATILLREEG 381
Qy 363 YPSVFGYDYG-----IPTHGVPAMKSKIDPLLOARQTFAYGTQHDYFDHDDIIGW 413
Db 382 YPSVFYADYGAQYSDKGYNNMAKVP---YIEELVTLRKEYAYGKQNSYLDHWDVLGW 437
Qy 414 TREGNSHPNSGLATIMSDGCGNKNMYVGNKAGQWRDITGNRTGTVTINADGHNFSV 473
Db 438 TREGDAEHPNS--MAVINSMDGPGGKMYTGPSTRYV--DKLGIRTEEVWTDANGAEFP 494
Qy 474 VNGGSVSVWV 483
Db 495 VNGGSVSVWV 504
```

```
RESULT 12
Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;
```

```
Query Match 49.5%; Score 1344; DB 2; Length 493;
Best Local Similarity 50.9%; Pred. No. 5.3e-79;
Matches 245; Conservative 75; Mismatches 153; Indels 8; Gaps 3;

Qy 6 NGTMMQYFEWYLPNDGNHNRRLDDAANLKS KGITAVMIPPAMKGTSONDVGYGAYDLYD 65
Db 4 NHTMMQYFEWHLAAGDGHKKLAEMAPELKAKGIDTVWPPVTKAVSAEDTGYGYDLYD 63

Qy 66 LGEPNQGTVRTKGTNRNLOAAVTS LKNGIQYGVGVMMHKGAGDTEIVNAVEVNR 125
Db 64 LGEPDQGTVRTKGTNRNLOAAVTS LKNGIQYGVGVMMHKGAGDTEIVNAVEVNR 123

Qy 126 NRQETSSEYAIETAWTKFDPGCGNNHSSPKRWYHFDGTDWDSRQLQNKIYKFRGTGK 185
Db 124 DRTKEISEPFEIETGWTFTPPGRDQYSSFKWNSHFNFTDFA--ARBERTGVFRAGENK 182

Qy 186 ADWEVDTEGNDYLMYADVMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHKYSF 245
Db 183 KWNENVDEGNDYLMYADVMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHKYSF 242

Qy 246 TRDWLTHVRNTTGKMFVAFWKNLGAENYLNKTSWNHVSFDPVPLHYNLYNASGG 305
Db 243 IKEFAEMIRKRGDQFYVGEFNSNLDACREFLDYDQIDLDVSLHYKLHEASLKR 302

Qy 306 YDMRNLINGSVQKHPTHAVTFVDNHDSPGEALESFVQVQWFKPLAYALVLTREQYPS 365
Db 303 DFOLSKIFDPTLVQTHPTHAVTFVDNHDSPGEALESFVQVQWFKPLAYALVLTREQYPS 362
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Qy 366 VFYGDYGI-----PTHGVPAMKSKIDPLLOARQTFAYGTQHDYFDHDDIIGWREGNSH 421
Db 363 VFYGDYGI-----KKEILDILLSARCNAKAYGEQEDYFDHANTIGWVRGVEEI 419
Qy 422 ENSGLATIMSDGCGNKNMYVGNKAGQWRDITGNRTGTVTINADGHNFSVNGGSVSV 481
Db 420 EGSCAVVISNGDGEKRMFGEHRAGEVWVDLTKSCDDQITIEDGWTATPHVCGGGVSV 479
Qy 482 W 482
Db 480 W 480

RESULT 13
Q89YP1 PRELIMINARY; PRT; 481 AA.
AC Q89YP1
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;
```

```
Query Match 49.0%; Score 1329; DB 16; Length 481;
Best Local Similarity 49.6%; Pred. No. 4.8e-78;
Matches 238; Conservative 86; Mismatches 154; Indels 2; Gaps 2;

Qy 6 NGTMMQYFEWYLPNDGNHNRRLDDAANLKS KGITAVMIPPAMKGTSONDVGYGAYDLYD 65
Db 3 NGVMMQYFEWHLNDGKLWKQIKEDALHLHDIGTAVWIPPAYKADQDEGYATYDLYD 62

Qy 66 LGEPNQGTVRTKGTNRNLOAAVTS LKNGIQYGVGVMMHKGAGDTEIVNAVEVNR 125
Db 63 LGEPDQGTVRTKGTNRNLOAAVTS LKNGIQYGVGVMMHKGAGDTEIVNAVEVNR 122

Qy 126 NRQETSSEYAIETAWTKFDPGCGNNHSSPKRWYHFDGTDWDSRQLQNKIYKFRGTGK 185
Db 123 ERTKALGEPFEIETGWTFTPPGRDQYSSFKWNSHFNFTDFA--QKRGVFIQIEGK 181

Qy 186 ADWEVDTEGNDYLMYADVMDHPEVIHELNRWGVYNTNLNLDGFRIDAVKHKYSF 245
Db 182 ANSEGVDSNGNDYLLCNDIDLDHPVSELNKGWNSNELNLDGFRIDAVKHKYSF 241

Qy 246 TRDWLTHVRNTTGKMFVAFWKNLGAENYLNKTSWNHVSFDPVPLHYNLYNASGG 305
Db 242 VAQFLDAVRGERGNDYVAVGEYVWNGDLLEADVAIEAVGHKVNLFDPVPLHYNMFQASQEGK 301

Qy 306 YDMRNLINGSVQKHPTHAVTFVDNHDSPGEALESFVQVQWFKPLAYALVLTREQYPS 365
Db 302 DYDLRDLKDTLVHEHHPDLAVTFVDNHDSPGEALESFVQVQWFKPLAYALVLTREQYPS 361

Qy 366 VFYGDYGI-----PTHGVPAMKSKIDPLLOARQTFAYGTQHDYFDHDDIIGWREGNSH 425
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Db 362 LFYGYDYGIKGEKSPHTRI-IDILLDARRKAYAGDQIEYFDHPSTIGFIRTGDEEHNGSG 420
Qy 426 LATIMSDPGGNKMYVGNKAGQWRDITGNRTGTVTINADGWNFSVNGSGSVVWVKQ 485
Db 421 LVFLMSNDEAGSKIMSLGKHKGEVWHEITGSISEITLDEEGNGBFSVESRLNAVWVK 480

RESULT 14
Q8DT08 PRELIMINARY; PRT; 486 AA.
AC Q8DT08;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UAI59 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UAI59, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL; AE014990; AAM59233.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; Alp_amyl_cat_sub.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;

Query Match 47.0%; Score 1274.5; DB 16; Length 486;
Best Local Similarity 48.8%; Pred. No. 1.6e-74;
Matches 236; Conservative 73; Mismatches 170; Indels 5; Gaps 4;

Qy 5 TNGTMQYFEWYLPNDGNHNRLRDDAANLKSQGITAVMIPPAAKGTSONDVGCGAYDLY 64
Db 2 TNETMQYFEWYLPNDGKHQHLAEDASHLKNIGISKVMPAPKGTGSDNDVGCGYVDLY 61

Qy 65 DLGFEFNQKGTVRTKYGTRNQLQAQVTSLKNGIQVYGDVVMNHKGGADGTEIVNAVENVNR 124
Db 62 DLGFEFNQGTVRTKYGSDREYLVANVNAKQEIPTSDIVLNKANGDAKERQVQVKNP 121

Qy 125 SNRQETSGBEYAEATWTKFDPGGRGNHNSFKRWYHFDGTDWDSQRLQNKIYKFRGTG 184
Db 122 SNRQEKISEPEYIEGWTQFPNPGRQDNYSDFKWHYHFTGVDYDALHN-ENGIYMLGDN 180

Qy 185 KAW--DWEVDVTENGNYYLMAVDMDHPEVIHELNRWGVYNTNMLDGFRLDAVKHIK 242
Db 181 KGWASQENIDQENGYDLYMDYDDIDFKHPEVQEHRLDWAFLFETSGVGGRFLDAKHID 240

Qy 243 YSFTRDLWTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNASN 302
Db 241 KTFMAQFIRYIREHLKADLVFGEGYWKDSHFDITDYLHSVDLQFDLLIDVMLHSLFEAQ 300

Qy 303 SGGYDVRNGLINGVQKQHPHTAVTFVDNHDSPGEALESFVQOQFKAVALVLTREQ 362
Db 301 KGSDFDLSTLLDSDLSMKSHDPFAVTFVDNHDSPGQALESTVAEVKFLAYGLILLRQEG 360

Qy 363 YPSVFGDYGVGIP-THGVPAWMSKIDPLQARQTFAGTQCHDYDHDHDIIGWTRGNSH 421
Db 361 IPCVFYGDYIGISGEFAQESFGQVILDKLLYRQTHVYGSQEDFPDYANCIGWICLGDDEH 420
```

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Qy 422 PNSGLATIMSDPGGNKMYVGNKAGQWRDITGNRTGTVTINADGWNFSVNGSGSVV 481
Db 421 PD-GVAIIISNGEANCCKRMNMGFEFNRNKFVVDYLNNTCTEVLDDQGWGDFPVOEASLSA 479

Qy 482 WVKQ 485
Db 480 WVNK 483

RESULT 15
Q8EOM2 PRELIMINARY; PRT; 488 AA.
AC Q8EOM2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha amylase family protein.
GN SAG0708.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Masiugnani V., Cielesiewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Masiugnani I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
DR EMBL; AE014223; AAM99595.1; -.
DR TIGR; SAG0708; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 56555 MW; 57249E354B2F053E CRC64;

Query Match 46.4%; Score 1259.5; DB 16; Length 488;
Best Local Similarity 47.5%; Pred. No. 1.5e-73;
Matches 229; Conservative 84; Mismatches 164; Indels 5; Gaps 4;

Qy 5 TNGTMQYFEWYLPNDGNHNRLRDDAANLKSQGITAVMIPPAAKGTSONDVGCGAYDLY 64
Db 2 TNELINQAFEWYLPDGNHKKLEESISDLKLGISKIWLPPAFKGTSSDDVGCGYVDLF 61

Qy 65 DLGFEFNQKGTVRTKYGTRNQLQAQVTSLKNGIQVYGDVVMNHKGGADGTEIVNAVENVNR 124
Db 62 DLGFEFNQGTVRTKYGRKEEYKLKLSKANGIKPFADIVLNHKGADHKEKFPQVVKNP 121

Qy 125 SNRQETSGBEYAEATWTKFDPGGRGNHNSFKRWYHFDGTDWDSQRLQNKIYKFRGTG 184
Db 122 ENRQEALSPYELEGWTFGDFPGRQGEYNDFKWHYHFTGLDYD-AKNNETDIFMIVGDN 180

Qy 185 KAW--DWEVDVTENGNYYLMAVDMDHPEVIHELNRWGVYNTNMLDGFRLDAVKHIK 242
Db 181 KGWADDLDDENGNDYLMYNDIDFKHPEVKNLQDWAKWFLETGTGIEGFRDLDAVKHID 240

Qy 243 YSFTRDLWTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNASN 302
```

Db 241 SYFIQTINDIRTKIKPDLEVPGEYWKSDQTSMDYLEATQFSLVDVTLHMNPFEDASH 300
Qy 303 SGGYIDMRNILLNGSVVQKHPTHAYTFVDNHDSPGEALESEFVQQWFKPLAYALVLTREQ 362
Db 301 QNRDFDMRTIFDDSLVIDNPEYATFVENHDTQSGQALSRVEDWFKPLAYGLILLRQOG 360
Qy 363 YPSVFIYGDYIGIP-THGVPAKSKIDPLLQAROTPAYGTQHDYFDHDDIIGWTREGNSSH 421
Db 361 TPCLFYGDYIYIGIYGFQGFQSPFKEVIDKMAELRQNYVFGKQVDYETHSNCIGWTCIGDBEH 420
Qy 422 PNSGLATIMSDGPGCKMWYVGNKAGQVWFDITGNRTGTVTINADGWNESVNGGVSU 481
Db 421 -NSCLAVVLINGDQGWKHMEVGEIYAGKTFVDYLGNCQEYVIGDDGWDGDFVESASISA 479
Qy 482 WV 483
Db 480 WV 481

Search completed: October 7, 2004, 00:18:54
Job time : 53.501 secs

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 15.0278 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-2
Perfect score: 2714
Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGKMFVSGSVVVRKQ 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2714	100.0	485	2	US-08-446-803-1
2	2714	100.0	485	2	US-08-861-837-1
3	2714	100.0	485	2	US-08-600-908A-12
4	2714	100.0	485	3	US-08-683-838A-12
5	2714	100.0	485	3	US-08-600-656-1
6	2714	100.0	485	3	US-09-170-670-1
7	2714	100.0	485	3	US-09-170-670-7
8	2714	100.0	485	3	US-09-193-068-1
9	2714	100.0	485	3	US-09-193-068-7
10	2714	100.0	485	3	US-09-183-412-1
11	2714	100.0	485	3	US-09-183-412-7
12	2714	100.0	485	3	US-09-354-191A-1
13	2714	100.0	485	4	US-09-291-023A-19
14	2714	100.0	485	4	US-09-290-734-1
15	2714	100.0	485	4	US-09-290-734-7
16	2714	100.0	485	4	US-09-636-252A-12
17	2714	100.0	485	4	US-09-381-687-2
18	2714	100.0	485	4	US-09-545-586-1
19	2714	100.0	485	4	US-09-545-586-7
20	2714	100.0	485	4	US-09-540-715A-19
21	2714	100.0	485	4	US-09-769-864-1
22	2714	100.0	485	4	US-09-769-864-1
23	2710	99.9	485	3	US-09-264-097-7
24	2699.5	99.5	486	4	US-09-381-687-4
25	2613	96.3	485	4	US-09-291-023A-18
26	2613	96.3	485	4	US-09-381-687-1
27	2613	96.3	485	4	US-09-540-715A-18

Qw
Search

28	2613	96.3	516	4	US-09-986-676A-2	Sequence 2, Appli
29	2448	90.2	485	2	US-08-446-803-2	Sequence 2, Appli
30	2448	90.2	485	2	US-08-861-837-2	Sequence 2, Appli
31	2448	90.2	485	3	US-08-600-656-2	Sequence 2, Appli
32	2448	90.2	485	3	US-09-170-670-2	Sequence 2, Appli
33	2448	90.2	485	3	US-09-170-670-8	Sequence 2, Appli
34	2448	90.2	485	3	US-09-193-068-2	Sequence 2, Appli
35	2448	90.2	485	3	US-09-193-068-8	Sequence 8, Appli
36	2448	90.2	485	3	US-09-183-412-2	Sequence 2, Appli
37	2448	90.2	485	3	US-09-183-412-8	Sequence 8, Appli
38	2448	90.2	485	3	US-09-264-097-5	Sequence 5, Appli
39	2448	90.2	485	3	US-09-354-191A-2	Sequence 2, Appli
40	2448	90.2	485	4	US-09-230-734-2	Sequence 2, Appli
41	2448	90.2	485	4	US-09-290-734-8	Sequence 8, Appli
42	2448	90.2	485	4	US-09-381-687-3	Sequence 3, Appli
43	2448	90.2	485	4	US-09-545-586-2	Sequence 2, Appli
44	2448	90.2	485	4	US-09-545-586-8	Sequence 8, Appli
45	2448	90.2	485	4	US-09-769-864-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-446-803-1
; Sequence 1, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Otttrup, Helle
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 5824531o No. 5824531disk of No. 5824531th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,803
; FILING DATE: 01-June-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-803-1

Query Match 100.0%; Score 2714; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 1.7e-229;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTNGTMQYFEWYLPNDGNHNRDDAANKSGITAVIIPPAWKGTSDNDVGYGA 60
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Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTSDNDVGYGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRNQLAAVTSKNGGIQVYGDVVMNHKGGADGTEIVNAV 120
Db 61 YDLYDLGEFNQKGTVRTKYGTRNQLAAVTSKNGGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAEATWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEATWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTPENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTPENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSNNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSNNHNSVDFVPLHYNLYNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSGSVS 480
QY 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 2

US-08-861-837-1
; Sequence 1, Application US/08861837
; Patent No. 5856164
; GENERAL INFORMATION:
; APPLICANT: Ottrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5856164o No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,837
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446, 803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-861-837-1

Query Match 100.0%; Score 2714; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTSDNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTSDNDVGYGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRNQLAAVTSKNGGIQVYGDVVMNHKGGADGTEIVNAV 120
Db 61 YDLYDLGEFNQKGTVRTKYGTRNQLAAVTSKNGGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAEATWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEATWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTPENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTPENGNYDLYMADVDMDHPEVHELNRNGWVYTNLTNLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSNNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDMLTHVRNTTGGKMFVAEAFKNDLGAENLYNKTSNNHNSVDFVPLHYNLYNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSGSVS 480
QY 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 3

US-08-600-908A-12
; Sequence 12, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989169o No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:


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APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-600-908A-12

Query Match      100.0%; Score 2714; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNNGTGTMQYFEWYLPNDGNHNRRLRDPDANKSKGITAVWIIPPAWKGTSONDVYGA 60
DB 1 HNNGTGTMQYFEWYLPNDGNHNRRLRDPDANKSKGITAVWIIPPAWKGTSONDVYGA 60
QY 61 YDLYDLGEFNQKGVTRTKYGRNQLQAAYVSLKNGIQYGDVYVNMHKGADGTEIYNAV 120
DB 61 YDLYDLGEFNQKGVTRTKYGRNQLQAAYVSLKNGIQYGDVYVNMHKGADGTEIYNAV 120
QY 121 EVNRSNRNQTSGEYALBMTKDFPGRGNHNSFKRWYHFDGTDMDQSRQLONKIYKF 180
DB 121 EVNRSNRNQTSGEYALBMTKDFPGRGNHNSFKRWYHFDGTDMDQSRQLONKIYKF 180
QY 181 RGCGKADMEVDIENGNYDYIMYADVMDHPEVTHELRNMGWYNTLNLNDFGRIDAVKH 240
DB 181 RGCGKADMEVDIENGNYDYIMYADVMDHPEVTHELRNMGWYNTLNLNDFGRIDAVKH 240
QY 241 IKYSFTDMLTHVANTTGKPMFAVAEFWKNDLGAIENTYLNKTSNMHSVFDVPLHYNL YNA 300
DB 241 IKYSFTDMLTHVANTTGKPMFAVAEFWKNDLGAIENTYLNKTSNMHSVFDVPLHYNL YNA 300
QY 301 SNSGGYIDMKNILNGSVVQKHPHTAVTFVDNHSQPEBALSFYQKFKPLAYALVLTRE 360
DB 301 SNSGGYIDMKNILNGSVVQKHPHTAVTFVDNHSQPEBALSFYQKFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMSKIDPLQARQTFAYGTOHDYFDHHDIIIGWTRBNSS 420
DB 361 QGYPSVFGDYGIPTHGVPAMSKIDPLQARQTFAYGTOHDYFDHHDIIIGWTRBNSS 420
QY 421 HPNSGLATIMSDFGKMKMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480
DB 421 HPNSGLATIMSDFGKMKMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 4
US-08-683-838A-12
Sequence 12, Application US/08683838A
Patent No. 6022724
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Franczen, Henrik
APPLICANT: Borchert, Tordben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6022724 of No. 6022724 of No. 6022724 of America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York

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STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-838A-12

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Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 HNNGTGTMQYFEWYLPNDGNHNRRLRDPDANKSKGITAVWIIPPAWKGTSONDVYGA 60
QY 61 YDLYDLGEFNQKGVTRTKYGRNQLQAAYVSLKNGIQYGDVYVNMHKGADGTEIYNAV 120
DB 61 YDLYDLGEFNQKGVTRTKYGRNQLQAAYVSLKNGIQYGDVYVNMHKGADGTEIYNAV 120
QY 121 EVNRSNRNQTSGEYALBMTKDFPGRGNHNSFKRWYHFDGTDMDQSRQLONKIYKF 180
DB 121 EVNRSNRNQTSGEYALBMTKDFPGRGNHNSFKRWYHFDGTDMDQSRQLONKIYKF 180
QY 181 RGCGKADMEVDIENGNYDYIMYADVMDHPEVTHELRNMGWYNTLNLNDFGRIDAVKH 240
DB 181 RGCGKADMEVDIENGNYDYIMYADVMDHPEVTHELRNMGWYNTLNLNDFGRIDAVKH 240
QY 241 IKYSFTDMLTHVANTTGKPMFAVAEFWKNDLGAIENTYLNKTSNMHSVFDVPLHYNL YNA 300
DB 241 IKYSFTDMLTHVANTTGKPMFAVAEFWKNDLGAIENTYLNKTSNMHSVFDVPLHYNL YNA 300
QY 301 SNSGGYIDMKNILNGSVVQKHPHTAVTFVDNHSQPEBALSFYQKFKPLAYALVLTRE 360
DB 301 SNSGGYIDMKNILNGSVVQKHPHTAVTFVDNHSQPEBALSFYQKFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMSKIDPLQARQTFAYGTOHDYFDHHDIIIGWTRBNSS 420
DB 361 QGYPSVFGDYGIPTHGVPAMSKIDPLQARQTFAYGTOHDYFDHHDIIIGWTRBNSS 420
QY 421 HPNSGLATIMSDFGKMKMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480
DB 421 HPNSGLATIMSDFGKMKMYVGNKAGQVWRDITGNRTGTVITNADGNGFSVNGGSVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 5
US-08-600-656-1

```

Sequence 1, Application US/0660056
Patent No. 6093562
GENERAL INFORMATION:
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: No. 60935620 No. 6093562disk of No. 6093562ch America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318-204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-600-656-1

Query Match 100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGTSONDVYGA 60
DB 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGTSONDVYGA 60
QY YDLVLDGEFNQKGVTRKYGTRNQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
DB 61 YDLVLDGEFNQKGVTRKYGTRNQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
QY 121 EVNRSNRNOETSGEYALEAWTKFDPFGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
DB 121 EVNRSNRNOETSGEYALEAWTKFDPFGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
QY 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIELRNNGWYNTNLNLDGFRIDA VKH 240
DB 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIELRNNGWYNTNLNLDGFRIDA VKH 240
QY 241 IKYSFTRLDLTHVNTTGGKPFVAABFWKNDLGALENYLNTKTSNMHSVFDVPLHYNL YNA 300
DB 241 IKYSFTRLDLTHVNTTGGKPFVAABFWKNDLGALENYLNTKTSNMHSVFDVPLHYNL YNA 300
QY 301 SNSGGYDMRNILNGSVVQKHPHTAAVTFVNDHDSQPEALLESFVQWFKPLAVALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTAAVTFVNDHDSQPEALLESFVQWFKPLAVALVLTRE 360
QY 361 QGYPSVFYGDYGGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRBGNSS 420
DB 361 QGYPSVFYGDYGGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRBGNSS 420
QY 421 HNSGLATIMSDGPGNKMVYVGKXKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

|||||
DB 421 HNSGLATIMSDGPGNKMVYVGKXKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 VVWVKQ 485
DB 481 VVWVKQ 485

RESULT 6
US-09-170-670-1
Sequence 1, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276-200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 1
LENGTH: 485
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-170-670-1

Query Match 100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGTSONDVYGA 60
DB 1 HNNGTGTMQYFEWYLPNDGNHNRRLDDAANKSKGITAWIPPAWKGTSONDVYGA 60
QY YDLVLDGEFNQKGVTRKYGTRNQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
DB 61 YDLVLDGEFNQKGVTRKYGTRNQLAAVTSLKNNGIQVYGDVVMNHKGADGTEIVNAV 120
QY 121 EVNRSNRNOETSGEYALEAWTKFDPFGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
DB 121 EVNRSNRNOETSGEYALEAWTKFDPFGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKF 180
QY 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIELRNNGWYNTNLNLDGFRIDA VKH 240
DB 181 RGTGKAMDWEVDTENGNVDYLMYADVMDHPEVIELRNNGWYNTNLNLDGFRIDA VKH 240
QY 241 IKYSFTRLDLTHVNTTGGKPFVAABFWKNDLGALENYLNTKTSNMHSVFDVPLHYNL YNA 300
DB 241 IKYSFTRLDLTHVNTTGGKPFVAABFWKNDLGALENYLNTKTSNMHSVFDVPLHYNL YNA 300
QY 301 SNSGGYDMRNILNGSVVQKHPHTAAVTFVNDHDSQPEALLESFVQWFKPLAVALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPHTAAVTFVNDHDSQPEALLESFVQWFKPLAVALVLTRE 360
QY 361 QGYPSVFYGDYGGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRBGNSS 420
DB 361 QGYPSVFYGDYGGIPTHGVPAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRBGNSS 420
QY 421 HNSGLATIMSDGPGNKMVYVGKXKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HNSGLATIMSDGPGNKMVYVGKXKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 VVWVKQ 485
DB 481 VVWVKQ 485

RESULT 7

US-09-170-670-7
; Sequence 7, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-7

Query Match 100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA	60
Db	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA	60
Qy	61	YDLYLGEFNOKGTVRTKYGRNQLQAQVTSKNGIQVYGDVVMNHKGGADGTEIYNAV	120
Db	61	YDLYLGEFNOKGTVRTKYGRNQLQAQVTSKNGIQVYGDVVMNHKGGADGTEIYNAV	120
Qy	121	EVNRSNRNQTSGEYAIKAWTKPDPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180
Db	121	EVNRSNRNQTSGEYAIKAWTKPDPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180
Qy	181	RGTKAWDEVDTEGNYDYLMYADVDMHDPEVHELKRWGWYNTNLDGFRIDAVKH	240
Db	181	RGTKAWDEVDTEGNYDYLMYADVDMHDPEVHELKRWGWYNTNLDGFRIDAVKH	240
Qy	241	IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHNLNA	300
Db	241	IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHNLNA	300
Qy	301	SNSSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360
Db	301	SNSSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360
Qy	361	QGYPVSFYGDYGIPTHGVPAMKSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS	420
Db	361	QGYPVSFYGDYGIPTHGVPAMKSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS	420
Qy	421	HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
Db	421	HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
Qy	481	VWVKQ 485	
Db	481	VWVKQ 485	

RESULT 8

US-09-193-068-1
; Sequence 1, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjrulff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-1

Query Match 100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA	60
Db	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA	60
Qy	61	YDLYLGEFNOKGTVRTKYGRNQLQAQVTSKNGIQVYGDVVMNHKGGADGTEIYNAV	120
Db	61	YDLYLGEFNOKGTVRTKYGRNQLQAQVTSKNGIQVYGDVVMNHKGGADGTEIYNAV	120
Qy	121	EVNRSNRNQTSGEYAIKAWTKPDPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180
Db	121	EVNRSNRNQTSGEYAIKAWTKPDPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180
Qy	181	RGTKAWDEVDTEGNYDYLMYADVDMHDPEVHELKRWGWYNTNLDGFRIDAVKH	240
Db	181	RGTKAWDEVDTEGNYDYLMYADVDMHDPEVHELKRWGWYNTNLDGFRIDAVKH	240
Qy	241	IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHNLNA	300
Db	241	IKYSFTRDWLTHVNTTCKPMFAVAEPKNDLGAIENTLNKTSWNHVSFVDFPLHNLNA	300
Qy	301	SNSSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360
Db	301	SNSSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360
Qy	361	QGYPVSFYGDYGIPTHGVPAMKSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS	420
Db	361	QGYPVSFYGDYGIPTHGVPAMKSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS	420
Qy	421	HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
Db	421	HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS	480
Qy	481	VWVKQ 485	
Db	481	VWVKQ 485	

RESULT 9

US-09-193-068-7
; Sequence 7, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjrulff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.

US-09-193-068-7

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Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60

QY 61 YDLYDLGEFNGKGTVRTKYGTRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120
DB 61 YDLYDLGEFNGKGTVRTKYGTRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120

QY 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
DB 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPEVIELRNWGVWYTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPEVIELRNWGVWYTNLTLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAIEYLNKTSWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAIEYLNKTSWNHVSFVDPVPLHYNLYNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360

QY 361 QGYPSVFGYGYGIPTHGVPAWKSKIDPLLOAROTPAYGTOHDYFDHDDIIGWTRGNSS 420
DB 361 QGYPSVFGYGYGIPTHGVPAWKSKIDPLLOAROTPAYGTOHDYFDHDDIIGWTRGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 VVWKQ 485
DB 481 VVWKQ 485

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RESULT 10

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US-09-183-412-1
; Sequence 1, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-183-412-1

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Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60

QY 61 YDLYDLGEFNGKGTVRTKYGTRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120
DB 61 YDLYDLGEFNGKGTVRTKYGTRNQLQAAVTSLKNGGIQVYGVVNMHKGADGTEIVNAV 120

QY 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
DB 121 EVNRSNRNOETSGEYAEAWTKFDFPGRGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPEVIELRNWGVWYTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTEGNYDYLAMYADVMDHPEVIELRNWGVWYTNLTLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAIEYLNKTSWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAIEYLNKTSWNHVSFVDPVPLHYNLYNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYDMRNILNGSVVQKHPTHAVTFVDNHDSDQGEALESFVQWFKPLAYALVLTRE 360

QY 361 QGYPSVFGYGYGIPTHGVPAWKSKIDPLLOAROTPAYGTOHDYFDHDDIIGWTRGNSS 420
DB 361 QGYPSVFGYGYGIPTHGVPAWKSKIDPLLOAROTPAYGTOHDYFDHDDIIGWTRGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 VVWKQ 485
DB 481 VVWKQ 485

```

RESULT 11

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US-09-183-412-7
; Sequence 7, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-7

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Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLVDLGEFNGKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120
Db 61 YDLVDLGEFNGKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120
Qy 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENLNKTSWNHVSFVDFPLHNLNA 300
Db 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENLNKTSWNHVSFVDFPLHNLNA 300
Qy 301 SNGSGYYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Db 301 SNGSGYYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAKMSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYDYGIPTHGVPAKMSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 12
US-09-354-191A-1
; Sequence 1, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728

```

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; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-354-191A-1

Query Match      100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLVDLGEFNGKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120
Db 61 YDLVDLGEFNGKGTVRTKYGRNQLQAATVSLKNGIQVYGVVNMHKGADGTEIVNAV 120
Qy 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDYLMDVMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENLNKTSWNHVSFVDFPLHNLNA 300
Db 241 IKYSFTRDWLTHVRNTTGKPMFAVAEPKNDLGAENLNKTSWNHVSFVDFPLHNLNA 300
Qy 301 SNGSGYYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Db 301 SNGSGYYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAKMSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYDYGIPTHGVPAKMSKIDPLLAQRTFAYGTOHDYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 13
US-09-291-023A-19
; Sequence 19, Application US/09291023A
; Patent No. 6309871
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoesck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0

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; SEQ ID NO 19
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus
US-09-291-023A-19

Query Match      100.0%; Score 2714; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60

Qy 61 YDLIDLGEFNGKQTVRTKYGTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIYNAV 120
Db 61 YDLIDLGEFNGKQTVRTKYGTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIYNAV 120

Qy 121 EVNRSNRNOETSGEYAEAWTKFDPGRGNHNSFKWRWYHFDGTDWDSRQLQNKIYKF 180
Db 121 EVNRSNRNOETSGEYAEAWTKFDPGRGNHNSFKWRWYHFDGTDWDSRQLQNKIYKF 180

Qy 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPHPEVIELRNKGVWYTTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPHPEVIELRNKGVWYTTNLDGFRIDAVKH 240

Qy 241 IKYSFTRDLTHVRNTTGKPMFAVAEFKNDLGAIEYLNKTSWNHNSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDLTHVRNTTGKPMFAVAEFKNDLGAIEYLNKTSWNHNSVFDVPLHYNLYNA 300

Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420
Db 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420

Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VWKQ 485
Db 481 VWKQ 485

RESULT 14
US-09-290-734-1
; Sequence 1, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus sp.
US-09-290-734-1

Query Match      100.0%; Score 2714; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60

Qy 61 YDLIDLGEFNGKQTVRTKYGTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIYNAV 120
Db 61 YDLIDLGEFNGKQTVRTKYGTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIYNAV 120

Qy 121 EVNRSNRNOETSGEYAEAWTKFDPGRGNHNSFKWRWYHFDGTDWDSRQLQNKIYKF 180
Db 121 EVNRSNRNOETSGEYAEAWTKFDPGRGNHNSFKWRWYHFDGTDWDSRQLQNKIYKF 180

Qy 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPHPEVIELRNKGVWYTTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPHPEVIELRNKGVWYTTNLDGFRIDAVKH 240

Qy 241 IKYSFTRDLTHVRNTTGKPMFAVAEFKNDLGAIEYLNKTSWNHNSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDLTHVRNTTGKPMFAVAEFKNDLGAIEYLNKTSWNHNSVFDVPLHYNLYNA 300

Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420
Db 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420

Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VWKQ 485
Db 481 VWKQ 485

RESULT 15
US-09-290-734-7
; Sequence 7, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PR1
; ORGANISM: Bacillus sp.
US-09-290-734-7

Query Match      100.0%; Score 2714; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-229;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60

Qy 61 YDLIDLGEFNGKQTVRTKYGTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIYNAV 120
Db 61 YDLIDLGEFNGKQTVRTKYGTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIYNAV 120

Qy 121 EVNRSNRNOETSGEYAEAWTKFDPGRGNHNSFKWRWYHFDGTDWDSRQLQNKIYKF 180
Db 121 EVNRSNRNOETSGEYAEAWTKFDPGRGNHNSFKWRWYHFDGTDWDSRQLQNKIYKF 180

Qy 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPHPEVIELRNKGVWYTTNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDLYMAYADVMDHPHPEVIELRNKGVWYTTNLDGFRIDAVKH 240

Qy 241 IKYSFTRDLTHVRNTTGKPMFAVAEFKNDLGAIEYLNKTSWNHNSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDLTHVRNTTGKPMFAVAEFKNDLGAIEYLNKTSWNHNSVFDVPLHYNLYNA 300

Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420
Db 361 QGYPSVFYGYGIPHTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNS 420

Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VWKQ 485
Db 481 VWKQ 485
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Db	61	YDYLDELGEFNOGKTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVNHNKGGADGTEIUNAV	120
Qy	121	EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF	180
Db	121	EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF	180
Qy	181	RGTCAMDWEVDTENGNYDYLAMYADVMDHPEVTHELRNNGVWYTNLTLDGFRIDAVKH	240
Db	181	RGTCAMDWEVDTENGNYDYLAMYADVMDHPEVTHELRNNGVWYTNLTLDGFRIDAVKH	240
Qy	241	IKYSFTRDLWLTHTVNTTGGKPMFAVAEFWKNDLGAIENYLNKTSWNHVSFVDPVPLHYNLYNA	300
Db	241	IKYSFTRDLWLTHTVNTTGGKPMFAVAEFWKNDLGAIENYLNKTSWNHVSFVDPVPLHYNLYNA	300
Qy	301	SNSGGYDMRNILNGSVVQKHPHTHATVFDVNDHSDQGEALESFVQOWFKPLAYALVLTRE	360
Db	301	SNSGGYDMRNILNGSVVQKHPHTHATVFDVNDHSDQGEALESFVQOWFKPLAYALVLTRE	360
Qy	361	QGYPSVFYGDYIGIPTHGVPAMKSKIDPLLOAROTFAYGTOHDYFDHHDIIIGWTREGNSS	420
Db	361	QGYPSVFYGDYIGIPTHGVPAMKSKIDPLLOAROTFAYGTOHDYFDHHDIIIGWTREGNSS	420
Qy	421	HPNSGLATINSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGNFSVNGGSVS	480
Db	421	HPNSGLATINSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGNFSVNGGSVS	480
Qy	481	VWVKQ 485	
Db	481	VWVKQ 485	

Search completed: October 7, 2004, 00:47:05
Job time : 17.0278 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.50628 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-2

Perfect score: 2714

Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGNGNFSVNGSVVWVKQ 485

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2440	89.9	518	1 AMT6_BACS7	P19571 bacillus sp
2	1905	70.2	512	1 AMY_BACLI	P06278 bacillus li
3	1892.5	69.7	549	1 AMY_BACST	P06279 bacillus st
4	1850	68.2	514	1 AMY_BACAM	P00692 bacillus am
5	1074	39.6	494	1 AMY2_SALTY	P26613 ealmonella
6	1049	38.7	495	1 AMY2_ECOLI	P26612 ealmonella
7	316	11.6	1196	1 AMYB_PASPO	P21543 paenibacill
8	305.5	11.3	421	1 AMYA_VIGMU	P17859 vigna mungo
9	294	10.8	440	1 AM3A_ORYSA	P27932 oryza sativ
10	289.5	10.7	551	1 AMT4_PSESA	P22963 pseudomonas
11	285	10.5	548	1 AMT4_PSEST	P13507 pseudomonas
12	270.5	10.0	435	1 AM3D_ORYSA	P27933 oryza sativ
13	269	9.9	713	1 CDGT_BACS8	P17692 bacillus sp
14	268	9.9	713	1 CDGT_BACS0	P05618 bacillus sp
15	266.5	9.8	719	1 AMYM_BACST	P19531 bacillus st
16	266	9.8	712	1 CDGT_BACS3	P09121 bacillus sp
17	265.5	9.8	427	1 AMY2_HORVU	P04063 hordeum vul
18	265	9.8	703	1 CDGT_BACS2	P31746 bacillus sp
19	261	9.6	368	1 AMY3_HORVU	P04747 hordeum vul
20	259	9.5	438	1 AM3B_ORYSA	P27937 oryza sativ
21	258.5	9.5	438	1 AMY1_HORVU	P00693 hordeum vul
22	257.5	9.5	413	1 AMY3_WHEAT	P08117 triticum ae
23	257	9.5	713	1 CDGT_BACSP	P30921 bacillus sp
24	256	9.4	429	1 AMY6_HORVU	P04750 hordeum vul
25	256	9.4	437	1 AM3C_ORYSA	P27939 oryza sativ
26	255	9.4	437	1 AM3E_ORYSA	P27934 oryza sativ
27	255	9.4	713	1 CDGU_BACCI	P43379 bacillus ci
28	254.5	9.4	428	1 AMY1_ORYSA	P17654 oryza sativ
29	248	9.1	710	1 CDGT_THETU	P26827 thermoanaer
30	247.5	9.1	718	1 CDGT_BACCI	P30920 bacillus ci
31	246.5	9.1	718	1 CDGT_BACSS	P31747 bacillus sp
32	242	8.9	528	1 AMY_BACCI	P08137 bacillus ci
33	239.5	8.8	443	1 AM2A_ORYSA	P27935 oryza sativ

ALIGNMENTS

RESULT 1

ID	AMT6_BACS7	STANDARD;	PRT;	518 AA.
AC	P19571;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amyase)			
OS	(Maltohexaoside-producing amylase) (Exo-maltohexaohydrolase).			
OC	Bacillus sp. (strain 707).			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1416;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.			
RX	MBDLINE=8816284; PubMed=3259152;			
RA	Takamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;			
RT	"Nucleotide sequence of the maltohexaoside-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to liquefying type alpha-amyases";			
RL	Biochem. Biophys. Res. Commun. 151:25-31 (1988).			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive maltohexaoside residues from the non-reducing chain ends.			
CC	-1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By similarity).			
CC	-1- PATHWAY: Starch degradation.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; M18862; AA22231.1; -.			
DR	PIR; A27705; A27705.			
DR	HSSP; P06278; 1VJS.			
DR	InterPro; IPR006589; Alp_amy1_cat_sub.			
DR	InterPro; IPR006047; Alpha_amy1_cat.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amyase; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.			
FT	SIGNAL 1 33			
FT	CHAIN 34 518			
FT	ACT SITE 269 269			
FT	ACT SITE 273 273			
FT	ACT SITE 366 366			
FT	ACT SITE 139 139			
FT	METAL 196 196			
FT	METAL 219 219			
FT	GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.			
FT	BY SIMILARITY.			
FT	BY SIMILARITY.			
FT	BY SIMILARITY.			
FT	CALCIUM 1 (BY SIMILARITY).			
FT	CALCIUM 2 AND SODIUM (BY SIMILARITY).			
FT	CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).			

P14014 bacillus li
P31797 bacillus st
P27941 oryza sativ
P31835 paenibacill
Q02905 aspergillus
Q02906 aspergillus
P10529 aspergillus
P21567 saccharomyc
P04830 paenibacill
P30292 aspergillus
P80099 thermotoga
O86956 thermotoga

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FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY) .
FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY) .
FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY) .
FT METAL 240 240 CALCIUM 2 (BY SIMILARITY) .
FT METAL 242 242 CALCIUM 2 (BY SIMILARITY) .
FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 518 AA; 59009 MW; 3A961B21612682C4 CRC64;
SIMILARITY)).
Query Match 89.9%; Score 2440; DB 1; Length 518;
Best Local Similarity 87.6%; Pred. No. 4.8e-159;
Matches 425; Conservative 32; Mismatches 28; Indels 0; Gaps 0;
QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLDDAANLKSIGTAVWIPPAWKGTQSMDVGYGA 60
DB 34 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKSIGTAVWIPPAWKGSQNDVGYGA 93
QY 61 YDLVDLGEFNQKGTIRYKTRNLOAAYTSKNGKIQVGDGVVNNHKGADGTETVNAV 120
DB 94 YDLVDLGEFNQKGTIRYKTRNLOAAYTSKNGKIQVGDGVVNNHKGADGTETVNAV 153
QY 121 EVNRSNRNQTSGEYATKPPGGRGNHSSFKWRVHFDGTDWDQSRQLQNKIYKF 180
DB 154 EVNPNRNQVETGTYTEATWTRFPDPRGNTHSSFKWRVHFDGTDWDQSRQLNRIYKF 213
QY 181 RGTOKADWEVDTEGNYDYLMYADVDMDHPPEVHILRNKGVWYTNLTLDGFRIDAVKH 240
DB 214 RGHGKAWDEVDTEGNYDYLMYADVDMDHPPEVHILRNKGVWYTNLTLDGFRIDAVKH 273
QY 241 IKYSFTDMLTHVNTTCKMPFAVAEFKNDLGNENYLNKTSWNHVSFVDFPLHYNLYNA 300
DB 274 IKYSFTDMLHNVHSATGKNNKFAVAEFKNDLGNENYLNKTSWNHVSFVDFPLHYNLYNA 333
QY 301 SNSGGYDMRNINGSVVQKHPTAVTFVDNHDSPQGEALLESFVQWFKPLAYALVLTRE 360
DB 334 SKSGNDYDMNINFGTVVQHPHSHAVTFVDNHDSPQGEALLESFVEWFKPLAYALVLTRE 393
QY 361 QGYPSVFYGYGIPTHGVPAKMSKIDPLLAQRTFAYGTQHDYFDHDIIGWTRGNS 420
DB 394 QGYPSVFYGYGIPTHGVPAKMSKIDPLLAQRTFAYGTQHDYFDHDIIGWTRGNTA 453
QY 421 HPNSGLATIMSDGPGKNNKAGVQWRDITGNRTGTGTINADGWNFGSVNGGSVS 480
DB 454 HPNSGLATIMSDGPGKNNKAGVQWRDITGNRTGTGTINADGWNFGSVNGGSVS 513
QY 481 VWVKQ 485
DB 514 IWVWK 518
RESULT 2
ID_1 AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase) (BLA).
GN AMYS OR AMYL
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=86111694; PubMed=2418011;
RX Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RA "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RA multiple amino acid replacements and molecular modelling.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
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RL J. Biochem. 98:1147-1156(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=861195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Shahhoseini M., Ziaei A.A., Ghaemi N., Pourbabeai A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.P., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372(1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Laoide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amylL, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442(1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2192788; PubMed=11997021;
RA Kandra L., Gyemant G., Remenyik J., Kovacszi G., Liptak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltotriose substrates.";
RL FEBS Lett. 518:79-82(2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RC STRAIN=ATCC 6598; PubMed=2394736;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Gaillardin C., Masson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
RP AND GLU-365.
RC STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
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RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Gaillardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RL modulation of its stability over a 50 degrees C temperature range.";
RN Protein Eng. 16:287-293(2003).
RP MUTAGENESIS OF TRP-292 AND VAL-315.
RX STRAIN=ATCC 27811;
RX MEDLINE=22797417; PubMed=12915728;
RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;
RT "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycosylation
RT activity.";
RL Protein Eng. 16:505-514(2003).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX STRAIN=ATCC 27811;
RX MEDLINE=95182462; PubMed=7877175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RT amylase at 2.2-A resolution.";
RL J. Mol. Biol. 246:545-559(1995).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98212915; PubMed=9551551;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Activation of Bacillus licheniformis alpha-amylase through a
RT disorder-->order transition of the substrate-binding site mediated
RT by a calcium-sodium-calcium metal triad.";
RN Structure 6:281-292(1998).
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.
RP MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkmenburg J.P., Bisgaard-Prantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase."
RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
RP HL62V/N219P/A238V/Q293S/N294Y.
RX STRAIN=ATCC 6598;
RX MEDLINE=22538505; PubMed=12540849;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
RT introduction of hydrophobic residues at the surface.";
RL J. Biol. Chem. 278:11546-11553(2003).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
CC liquefaction of starch-containing washes and in the detergent
CC industry to remove starch. Sold under the name Termamyl by
CC Novozymes.
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
CC values (up to pH 11) and at high temperatures (up to 100 degrees
CC Celsius).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; X03236; CAA22681.1; --
DR EMBL; M38570; AAA22226.1; --
DR EMBL; M13256; AAA22240.1; --
DR EMBL; K01984; AAA22193.1; --

DR EMBL; AF438149; AAO26743.1; --
DR EMBL; M26412; AAA22237.1; --
DR EMBL; A17930; CAA01355.1; --
DR PIR; A91997; ALBSL.
DR PDB; 1BLI; 23-MAR-99.
DR PDB; 1BPL; 17-AUG-96.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR PDB; 1O80; 03-APR-03.
DR PDB; 1VJ5; 12-MAR-97.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 512 ALPHA-AMYLASE.
FT ACT_SITE 260 260
FT ACT_SITE 264 264
FT ACT_SITE 357 357
FT METAL 133 133
FT METAL 190 190
FT METAL 210 210
FT METAL 212 212
FT METAL 223 223
FT METAL 229 229
FT METAL 231 231
FT METAL 233 233
FT METAL 233 233
Query Match 70.2%; Score 1905; DB 1; Length 512;
Best Local Similarity 68.9%; Pred. No. 1.3e-122; Indels 10; Gaps 4;
Matches 334; Conservative 65; Mismatches 76;
Qy 6 NGTMMQYFEWYLPNDGNNRRLDDAANKSKGITAVIPPAWPKGTQNDVGVGAYDLYD 65
Db 33 NGTLMQYFEWYMPNDGQHWKRLQNDASAYLAEGHGTAVIPPAWPKGTQADVGVGAYDLYD 92
Qy 66 LGFBNQKGTVRTKGTNRNLOAAVTSKNGIOYGVGVVNNHKGAGDTEIVNAVENRS 125
Db 93 LGFBHQKGTVRTKGTNGELQSAIKSLHSRDINVGVDWINHKGADATEDVTAVEVDP 152
Qy 126 NRQOETSGEYAIKAWTKFDPFGSGNNHSSFKWYHFDGTDWQSRQLQNKIKYKFGT 185
Db 153 DRNRVISGEHRIKAWTHFHPFGSGTYSDFKWHYHFDGTDWDSRKL-NRIYKFPQ--GK 209
Qy 186 ADWEVDVTENGNDYLMYADVDMDHPEVIHELNRNWGVYTTNMLDGFRIIDAVKHKYSF 245
Db 210 ADWEVSNENGNDYLMYADIDYDHPDVAEIKRWGTWYANELQLDGFRLDAVKHKFSF 269
Qy 246 TRDWLTHVRNTTGKMPFAVAEFWKNDLGALENYLNKTSWNHNSVDFVPLHNLNNSGG 305
Db 270 LRDWNVHREKTKGKMTVAEYQNDLGALENYLNKTSWNHNSVDFVPLHNLNNSGG 329
Qy 306 YDMRNILNLSVYQKHPTHTAVTFVDNHSOPGEALSFVQWFKPLAYALVLTRECVPS 365
Db 330 GYDMRKLLNVTYVSKHPLKAVTFVDNHDTPQGSLESTVQTFWFKPLAYALVLTRECVPS 389
Qy 366 VFYGDYVYGIPTHG-----VPAMSKIDPLQARQTFAVGTQHDYFDHHDIIIGTREGNSS 420
Db 390 VFYGDWVG--TKGDSQREIPALKKHKEPILKARKQYAGAHQHDYFDHHDIVGTREGDSS 447
Qy 421 HPNSGLATIMSDGPGGNKMYGVGNKAGQVVRDITGNRTGTVTINADGWNFSVNGSGVS 480
Db 448 VANSGLAALITDGGGAKRMVGVGRQNAETGHTDITGNRSPVWINSEGVSEFHVNGSGVS 507
Qy 481 VVKVQ 485
Db 508 IYVQR 512

Db 159 DRQEIISGTTQIQWTFKDFPGRNTYSSFAWRWYHFDGVDWDSRKL-SRIYKFRIGK 217
Qy 186 AWDWEVDTEGNGDYLMYADYMDHPEVIHELNRWGVYNTLNLGDFRIDAVKHIFYSF 245
Db 218 AWDWEVDTEGNGDYLMYADYMDHPEVITELKSGKWKYVNTNIDGFRDLDAVKHIFSF 277
Qy 246 TRWLTHVRNTGKPMFAVAFKNDLGCATENYLNKTSWNHVSFDPVPLHYNLYNASHSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYSYDINKLHNYIMKTNGTMSLFDAPLHNFYTSKSGG 337
Qy 306 YYDMRNILNGSVVOKHPTHTVFDNHDSPGEALSFVQOQFKPLAYALVLTREOQVPS 365
Db 338 TFDNRILMTWYLMKQDTLAVTFVDNHDTEPCQALQSWDPWFPLAYAFILTRQEGYPC 397
Qy 366 VFYGDYVIGPTHGVPMKSKIDPLQAROTPAYCTQHDYFDHDDIIGWTREGNSHPNSG 425
Db 398 VFYGDYVIGPTHGVPMKSKIDPLQAROTPAYCTQHDYFDHDDIIGWTREGVTEKPGSG 457
Qy 426 LATIMSDPGNGKMYGKKGAGQVWRDITGNRTGTTINADGNGFVNGGVSVMVW 483
Db 458 LAALITDPGSGKMYGKKGAGQVWRDITGNRTGTTINADGNGFVNGGVSVMVW 515

RESULT 4

AMY_BACAM STANDARD; PRF; 514 AA.
AC P00692;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
OS Bacillus amyloliquefaciens.
OX Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Petersson R.F., Kalkkinen N., Palva I., Soederlund H.,
Kaeerlaeinen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RP SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Petersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
Soederlund H., Takkinen K., Kaeerlaeinen L.;
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkmenburg J.P., Bisgaard-Prantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase."

RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; J01542; AAA22191.1; -;
DR EMBL; V00092; CAA23430.1; -;
DR EMBL; A20154; CAA01489.1; -;
DR EMBL; M18424; AAA22192.1; -;
DR PIR; A92389; ALBSN.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006047; Alpha_aml_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW SIGNAL; 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 514 ALPHA-AMYLASE.
FT ACT_SITE 262 262
FT ACT_SITE 292 292
FT ACT_SITE 359 359
FT METAL 133 133
FT METAL 190 190
FT METAL 212 212
FT METAL 214 214
FT METAL 225 225
FT METAL 231 231
FT METAL 233 233
FT METAL 235 235
FT METAL 266 266
FT METAL 331 331
FT METAL 438 438
FT METAL 461 461
FT CONFLICT 54 54 L -> I (IN REF. 2).
FT CONFLICT 64 64 I -> L (IN REF. 2).
FT CONFLICT 79 79 S -> D (IN REF. 2).
FT CONFLICT 84 84 G -> S (IN REF. 2).
SQ SEQUENCE 514 AA; 58403 MW; 3DE66B3FB5CCDE7E CRC64;
Query Match 68.2%; Score 1850; DB 1; Length 514;
Best Local Similarity 66.4%; Pred. No. 7.3e-119;
Matches 324; Conservative 68; Mismatches 88; Indels 8; Gaps 3;
Qy 3 NGTNGTWQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSQNDVGYGAYD 62
Db 30 SAVNGTLMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSQNDVGYGAYD 89
Qy 63 LYDLGFEFNQGTVTYKTRNQLQAATVSLKNGIQTGYGVVMMHKGADTEINAVEV 122
Db 90 LYDLGFEFNQGTVTYKTRNQLQAATVSLKNGIQTGYGVVMMHKGADTEINAVEV 149
Qy 123 NRSNRNQTSEYAIKAWTKDFPFGNGNHSFKRWYHFDGTDWDSRQLQNKYKPRG 182
Db 150 NPANRNQTSEYAIKAWTKDFPFGNGNHSFKRWYHFDGTDWDSRQLQNKYKPRG 208

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QY 183 TCGKAWDEVDTEGNYDYLADVDMDHDPVIELRNKGWVYNTNLNLDGFRIDAVKHK 242
Db 209 EKGAWDEWSSNGNYDYLADVDYDHPVVAETKKGWYANELSLDGRIDAAKHK 268
QY 243 YSFTRDWLTHVNTTKGPFVAEAFWKNLGAENLNKTSWNHGSVDVPLHYNLYNASN 302
Db 269 FSLRDVQAVRAQATGKEMFTVAETWQNNAGLENLNKTSFNQSVFVPLHNLQAASS 328
QY 303 SGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTREQ 362
Db 329 QGGYDMRLLDGTVSRHPEKAVTFVENHDDTPQGSLESTVQWFKELAYAFILTRSG 388
QY 363 YPSVFGYDYGIPTHG-----VPAMKSKIDPLQLQARQTFAYGTHQYDHDHDIIGWTREG 417
Db 389 YPQVFGYDYG-----TRGTSFKPISPKDNIEPILKARKEYAYGPQHDYIDHDPVIGWTREG 446
QY 418 NSSHPNSGLATIMSDPGCNKMWYGVKNKAGQVWRDITGNRTGTVTNADGWNFSVNGG 477
Db 447 DSSAAKSGLAALITDPGGSKRYAGLNKAGETWYDITGNRSDDTVKIGSDGNGEFTVNDG 506
QY 478 SVSVMVKQ 485
Db 507 SVSIYVQK 514

RESULT 5
AMY2_SALTY
ID AMY2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR STM1963.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SJW1103;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=SJW1103;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [4]
RP SEQUENCE OF 476-494 FROM N.A.
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIb, including a

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RT large non-coding region."
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L01643; AAA27110.1; -.
CC DR EMBL; AE008787; AAL20875.1; -.
CC DR EMBL; M85241; AAA27079.1; -.
CC DR EMBL; L13280; AAA71970.1; -.
CC DR PIR; B45738; B45738.
CC DR HSP; P06278; IVJ8.
CC DR StyGene; SG10011; amyA.
CC DR InterPro; IPR006589; Alp_amy1_cat_sub.
CC DR InterPro; IPR006047; Alpha_amy1_cat.
CC DR Pfam; PF00128; alpha-amylase; 1.
CC DR SMART; SM00642; Amy; 1.
CC KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
FT SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5B47C CRC64;

Query Match 39.6%; Score 1074; DB 1; Length 494;
Best Local Similarity 42.7%; Pred. No. 5e-66;
Matches 210; Conservative 80; Mismatches 184; Indels 18; Gaps 6;

QY 6 NGTMQYFEWYLPNDGNHNRLRDDAANKSGITAVWIPPAWKGTSON-DVGYGAYDLY 64
Db 3 NPTLLQYFHWYVPDGGKLSWSELAERADGLDIGINWVLPACKGASGGYSGYDYDLF 62
QY 65 DLGEFNQKGTVTKYGRNQLQAATVSLKNGIQYGVDMVNMHKGADGTEIVNAVEVNR 124
Db 63 DLGEFDQKGTATKYGRQLLTALDALKKNIAVLDDVVVNMHKGADGTEIVNAVEVNR 122
QY 125 SNRNQETSCEYAIETAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIKYKFRG-- 182
Db 123 DRTQIDNNIIECEWTRYTFPARAGYSNFVDFHCFSGDIDHENPD-EDGIFKIVNDY 181
QY 183 TCGKAWDEVDTEGNYDYLADVDMDHDPVIELRNKGWVYNTNLNLDGFRIDAVKHK 242
Db 182 TGDGWNDDQVDDMGNFYLMGENIDFRNHAVTEEEKYWARWVMEQTHCDGFLDAVKHIP 241
QY 243 YSFTRDWLTHVNTTKGPFVAEAFWKNLGAENLNKTSWNHGSVDVPLHYNLYNASN 302
Db 242 AMFYKEWIEHVQAVAPKPLFVAEYWSHEVDKLOTYIDQVDGKTMFLDPAQMKPFHEASR 301
QY 303 SGGYDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTREQ 362
Db 302 QCAEYDMRHIFFTGLVLEADPPHATLVANHDTPQLQALEAPVPEWFKPLAYALILRENG 361
QY 363 YPSVFGYDYGIPTH-----GVPAMKSKIDPLQLQARQTFAYGTHQYDHDHDI 411
Db 362 VPSVEYDLYGASVEDSGENGECRCVDMFVI-NQLDRLILARQRFAGHGIQTLFFDHPNCI 420
QY 412 GWTREGNSHNSGLATIMSDPGCNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWN 471

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QY 472 FSVNGGSVSVVW 483
Db 479 FFCNGGSVSVVW 490

RESULT 7
AMYB_PABPO
ID AMYB_PABPO STANDARD; PRT; 1196 AA.
AC P21543;
DC 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);
DE Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RA KAWAZU T., NAKANISHI Y., UOZUMI N., SASAKI T., YAMAGATA H.,
RA Tsukagoshi N., Udaoka S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RA MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Udaoka S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RA MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RA MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Udaoka S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amylase.";
RL Biochemistry 30:4594-4599(1991).
CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
CC SECRETION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC -----
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CC -----
CC EMBL; M15817; AAA85446.1; -;
CC EMBL; Y00150; CAA68344.1; -;

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DR PIR; A29130; A29130.
DR HSSP; P36924; 1B9Z.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR005085; CBM_25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR001554; Glyco_hydro_14.
DR Pfam; PF001128; alpha-amylase; 1_14.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF03423; CBM_25; 2.
DR Pfam; PF01373; Glyco_hydro_14; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00750; BETAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C; 1.
DR PROSITE; PS00506; BETA_AMYLASE_1; 1.
DR PROSITE; PS00679; BETA_AMYLASE_2; 1.
DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
FT DOMAIN 36 454 BETA-AMYLASE.
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196
FT DISULFID 118 126
FT ACT_SITE 198 198
FT ACT_SITE 394 394
FT MUTAGEN 118 118
FT MUTAGEN 126 126
FT MUTAGEN 358 358
FT CONFLICT 1 1
FT CONFLICT 67 67
FT CONFLICT 100 100
FT CONFLICT 154 154
FT CONFLICT 177 177
FT CONFLICT 227 228
FT CONFLICT 330 330
FT CONFLICT 425 425
FT CONFLICT 493 493
FT CONFLICT 532 532
FT CONFLICT 559 559
FT CONFLICT 665 665
FT CONFLICT 681 681
FT CONFLICT 686 686
FT CONFLICT 725 728
FT CONFLICT 736 736
FT CONFLICT 741 741
FT CONFLICT 758 758
FT SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;
Query Match 11.6%; Score 316; DB 1; Length 1196;
Best Local Similarity 23.9%; Pred. No. 6e-14;
Matches 124; Conservative 68; Mismatches 189; Indels 138; Gaps 25;
QY 1 HENGTTGTMMQYFEWLPNDGNHNRRLRDAANLAKSKGTAVWIPPAWKGTQNDV-GYG 59
Db 766 NYGGFNNSNDQKRWK-----GGDFQGIINKLDYIKRMGFTAIWTPVTKQSEYAHGYH 821
QY 60 AYLDYDLGFEFNQGTVRTKYGTRNQLQAAVTSLKKNIGIQVYGDVVMNHKGGADGTEIVNA 119
Db 822 TYDFY-----AVDGHGLGTMKQLQELVRKAHDKNIAVMVDVVVNHGT----- 862
QY 120 VEVNRSNRNQETSGEYATEAWTKDFP-PCRGNNSHF-KRWYHFDG--TDWDQSRQLQN 175
Db 863 -----DFQPGNGFAKPFDDKADWYHHNGDITDGDYNSNNQ- 897
QY 176 KIYKFRGTGKAMDWEVDTEGNYDYLMYADVMDHPEVTHELRNMGVWYTNLTNLDGPR 235
Db 898 -----WKI--ENG--DVAGLDDLHNENPATANELKNWIKWLLNETGIDGLRL 940
QY 236 DAVKHKYSFTRDMLTHVRNTTGTGKPMFAVEAPFWKNDLGAIEYNLKNKTSWNHVSFDPPLHY 295

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Db 941 DTVKHVKGLKDF-DOAANT-FTMGIEFHGDPAYVGDY-TRYLDAALDFPMY 991
QY 296 NLVNASGGYDMRNLTNGSVQKHPTAVT-FVDNHD-SOPGEALESF 343
Db 992 TIKDV-FGHDSKRIKDRYSDDRYRDAQTNGVFDNHDVRFNDASGKPGANYDKW 1049
QY 344 VQWFKPLAYALVLT-REQVPSVFYGDYIGPHTHGVPMKSKIDPLQLAROTTFAYGTQH 402
Db 1050 PQ-----LKAALGFTLTSRGIPFIYQGTQEGYSGDDPA-----NRENNFNANH 1094
QY 403 DYFDHDDIIQWTRGNSHSHNSGLATIMSDPGCNKWM-----YVGKNKAG-----Q 449
Db 1095 DLYQYIAKLNYR---NNHP-----ALQNSQREKWDVDSFYSFQSKNGDEAIVFINN 1145
QY 450 VWRDIT---GN-----RGTVTINADGNGFNSVNGSVSV 481
Db 1146 SWSNQTFTIGNFNLNGTTLNQLNSDVSQVINGNSITV 1184

RESULT 8
AMYA VIGMU STANDARD; PRT; 421 AA.
AC F17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (Black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3915;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RT "Nucleotide sequence of cDNA for alpha-amylase from cotyledons of
terminating Vigna mungo seeds."
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2];
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo."
RL Plant Physiol. 103:1459-1459(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -I- COPACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC EMBL; X53049; CAA37217.1; -
DR EMBL; X73301; CAA51734.1; -
DR PIR; S10514; S10514.
DR HSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alp_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.

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KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT CHAIN 1 23 PROBABLE.
FT ACT_SITE 24 421 ALPHA-AMYLASE.
FT ACT_SITE 201 201 BY SIMILARITY.
FT ACT_SITE 309 309 BY SIMILARITY.
FT METAL 113 113 BY SIMILARITY.
FT METAL 130 130 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 149 149 CALCIUM 2 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
SQ SEQUENCE 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;

Query Match 11.3%; Score 305.5; DB 1; Length 421;
Best Local Similarity 25.6%; Pred. No. 9.1e-14;
Matches 100; Conservative 54; Mismatches 141; Indels 95; Gaps 15;

QY 9 MMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPMKGTSONDVGYGAYDLYDLGE 68
DB 26 LFQGFNWESSKKGWYNSLNSIPDLANAGITHVWLPSPQSVSPE--GYLPGRLYDL- 82
QY 69 FNQKGTVRTKYGRNOLQAAVTSKNGNGIOVYGVVNVNKHGG--ADGTEIVNAVEVNRSN 126
DB 83 -----ASKYGSKNELKSLIAAFHEKGIKCLADIVINHRTAEKRGDIYCIPEGGTPD 135
QY 127 RNQETSGEYAIETAWTKFDFEGRGNHNSFKRWYHFDGTDMQDSRQLQNKIYKFRGTGKA 186
DB 136 SRQDWGSPFCRDDTAYS-DGTGNDS-----GEG 164
QY 187 WDWEVDTEGNYDLYMAYDVMDH--PEVHELBNWGVWYNTNLNDGFRIDAVKHLKYS 244
DB 165 YD-----AAPDIDLNPQVQRELSMMNLKLTGIFDGFGRWDFYKGYAPS 209
QY 245 FTRDLWLTHTVNTTKPMFAVAEFW-----KNDLGAIEINLYNKTSWNHSVF 289
DB 210 ISKIYMQT-----KPDFAVGEKWDSSISYQDGKPNYNQDSHRGALVNVVESAGGATAP 264
QY 290 DVPLHLYNLNASGGYDMRNLTNGSVQKHPTAVT-FVDNHD-SOPGEALESF--- 343
DB 265 DFTTK-GILQAAVQGLWRLID-PNGKPPGMIGVKPENAVTFIDNHDGTSTQRLWPPFSD 322
QY 344 -VQWFKPLAYALVLTREQVPSVFYGDY. 372
DB 323 KVMQ-----GYAVILT-HPGTPSIFYDHF 346

RESULT 9
AM3A ORYSA STANDARD; PRT; 440 AA.
ID AM3A ORYSA
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
glucan glucanohydrolase).
DE AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etisolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice."
RL Plant Mol. Biol. 16:579-591(1991).

```

CC -!- FUNCTION: Important for breakdown of endosperm starch during germination.

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

CC -!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).

CC -!- SUBUNIT: Monomer.

CC -!- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.

CC -!- DEVELOPMENTAL STAGE: Expressed at a high level during germination in the aleurones cells under the control of the plant hormone gibberellic acid and in the developing grains at a low level.

CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

DR EMBL; X56336; CAA39776.1; -.

DR PIR; S14958; S14958.

DR HSP; P04063; LAVA.

DR Gramene; P27932; -.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amy1ase; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR SMART; SM00642; Amy; 1.

CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal; Multigene family.

CC SIGNAL 1 26

CC CHAIN 27 440

CC ACT_SITE 207 207

CC ACT_SITE 315 315

CC ACT_SITE 119 119

CC METAL 145 145

CC METAL 155 155

CC METAL 166 166

CC METAL 169 169

CC METAL 170 170

CC METAL 171 171

CC METAL 174 174

CC METAL 176 176

CC SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 10.8%; Score 294; DB 1; Length 440;

Best Local Similarity 25.8%; Pred. No. 5.8e-13;

Matches 106; Conservative 55; Mismatches 152; Indels 98; Gaps 19;

QY 9 MMQYFEW-YLPNDGNHNRURDAAALKSGITAVIIPPAWKGTSQNDVGYGAYDYLGL 67

DB 31 LFQGFNWSKKGQWYMLKQVGDIASGVTHVLPPTTHSVSPQ--GYMPGRLYDLN 88

QY 68 EFNQKGTVRTKYTRNQLQAQVTSKNGIQVYGVDMHKGADGTEIVNAVEVRSNR 127

DB 89 -----ASKYGTAKLSLIAFAAKGKVCDAIVNHRCADD----- 125

QY 128 NQTSGEYATKFWDFPGRGNHNSFKRWYHFDGTDMDQSRQLQNKIYKPGTGKAW 187

DB 126 -KDRGVYCI-----FKGGPRGC-----LDWGPSMICDDTQYSDGTHR- 165

QY 188 DWEVDTEGNYDYLMYADVMDHPEVIELRNNGVWYTNFLDGPRIIDAVKHIKYSFTR 247

DB 166 -----DT---GADFAAAPDIDHLPVQLQRELSDLRLWLRDVGDFGWRDLFAKGYSAVAR 218

QY 248 DWLTHVRNTTGKMPFAVEPKNKDLG-----AIENYLNKTSNHSVFDV 291

DB 219 ----TYQN--ARPSFVVAEIIW--NSLSYDGDGKPAANQDQGRQBLVNWVKGVGGFATADF 272

QY 292 PLHYNLYNASNGYDMRNILNG----SVVQKHPTAVTFVDNHDSPGSALESFVQWF 348

DB 273 TTK-GILQSAVQGBELWEMRD-KDGKAPGMIGWYPERKAVTFVDNHD-----GSTQRMWP 324

QY 349 KP-----LAVLVLTREQSPVSYFYGYGIPTHGVPAKSKIDPLQARQ 394

DB 325 FPSDKVLGYAYILT-HPGVPCIFYDQVFDW-----NLKQEIINALAATRK 368

RESULT 10

AMT4_PSESA

ID AMT4_PSESA STANDARD; PRT; 551 AA.

AC P22963;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-amy1ase) (Maltotetraose-forming amy1ase) (Exo-maltotetrahydrolase)

DE (Maltotetraose-forming exo-amy1ase).

GN MTA.

OS Pseudomonas saccharophila.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Comamonadaceae.

OX NCBI_TaxID=304;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IAM 1504;

RX MEDLINE=90005970; PubMed=2676600;

RA Zhou J., Baba I., Takano T., Kobayashi S., Arai Y.;

RT "Nucleotide sequence of the maltotetrahydrolase gene from Pseudomonas saccharophila.";

RL FEBS Lett. 255:37-41(1989).

CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive maltotetraose residues from the non-reducing chain ends.

CC -!- COFACTOR: Binds 2 calcium ions per subunit (By similarity).

CC -!- PATHWAY: Starch degradation.

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

CC -----

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CC -----

DR EMBL; X16732; CAA34708.1; -.

DR PIR; S05667; S05667.

DR HSP; P13507; 2AMG.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR002044; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amy1ase; 1.

DR Pfam; PF00686; CBM 20; 1

DR PRINTS; PR00110; ALPHAAMYLASE.

DR ProDom; PD001568; CBD 4; 1.

CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding; Signal.

CC SIGNAL 1 21

CC CHAIN 22 551

CC ACT_SITE 214 214

CC ACT_SITE 240 240

CC ACT_SITE 315 315

CC METAL 22 22

CC METAL 23 23

CC METAL 34 34

CC METAL 37 37

CC METAL 38 38

GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

CALCIUM 2 (BY SIMILARITY).

FT METAL	23	CALCIUM 2 (VIA CARBONYL OXYGEN).	FT TURN	380	381
FT METAL	34	CALCIUM 2.	FT STRAND	383	387
FT METAL	37	CALCIUM 2.	FT STRAND	393	398
FT METAL	38	CALCIUM 2.	FT STRAND	403	408
FT METAL	137	CALCIUM 1.	FT HELIX	415	417
FT METAL	172	CALCIUM 1.	FT TURN	418	418
FT METAL	175	CALCIUM 1. (VIA CARBONYL OXYGEN).	FT STRAND	424	429
FT METAL	183	CALCIUM 1.	FT TURN	430	433
FT METAL	218	CALCIUM 1 (VIA CARBONYL OXYGEN).	FT STRAND	434	438
FT DISULFID	161		SQ SEQUENCE	548 AA;	59876 MW; 2B87217B3379158F CRC64;
FT DISULFID	237				
FT CONFLICT	286				
FT TURN	28	GSIAADWKHGLNGNDPR -> ARSPTGSTRQSRPA (IN			
FT TURN	34	REF. 1).			
FT STRAND	34				
FT TURN	40				
FT TURN	46				
FT HELIX	48				
FT TURN	53				
FT HELIX	56				
FT TURN	63				
FT HELIX	64				
FT TURN	70				
FT STRAND	74				
FT STRAND	87				
FT TURN	90				
FT STRAND	92				
FT TURN	99				
FT STRAND	108				
FT TURN	109				
FT STRAND	111				
FT HELIX	113				
FT TURN	127				
FT STRAND	129				
FT STRAND	138				
FT TURN	141				
FT TURN	152				
FT STRAND	157				
FT HELIX	158				
FT STRAND	169				
FT TURN	170				
FT STRAND	172				
FT TURN	179				
FT TURN	181				
FT STRAND	183				
FT TURN	186				
FT HELIX	189				
FT STRAND	208				
FT HELIX	216				
FT TURN	221				
FT STRAND	236				
FT TURN	245				
FT HELIX	250				
FT HELIX	253				
FT TURN	259				
FT TURN	271				
FT STRAND	274				
FT HELIX	277				
FT HELIX	288				
FT HELIX	295				
FT HELIX	301				
FT TURN	305				
FT STRAND	307				
FT TURN	314				
FT HELIX	322				
FT HELIX	333				
FT HELIX	336				
FT STRAND	349				
FT HELIX	354				
FT TURN	359				
FT HELIX	363				
FT TURN	377				

FT TURN	380	381	TURN	380	381
FT STRAND	383	387	STRAND	383	387
FT STRAND	393	398	STRAND	393	398
FT STRAND	403	408	STRAND	403	408
FT HELIX	415	417	HELIX	415	417
FT TURN	418	418	TURN	418	418
FT STRAND	424	429	STRAND	424	429
FT TURN	430	433	TURN	430	433
FT STRAND	434	438	STRAND	434	438
SQ SEQUENCE	548 AA;	59876 MW; 2B87217B3379158F CRC64;	SQ SEQUENCE	548 AA;	59876 MW; 2B87217B3379158F CRC64;

Query Match 10.5%; Score 285; DB 1; Length 548;
Best Local Similarity 25.3%; Pred. No. 3.1e-12;
Matches 135; Conservative 66; Mismatches 151; Indels 182; Gaps 30;

QY	2	HNGTNGTMOYFEWYL----	PNDGNHNRRLRDDAANKSGITAVITPPPAWKTSQNDVG	57
DB	33	YHGGDEILLOGFHNNVREAPND--	WYNILRQQAATIAADGFSATWIPVWRDFSSWSDG	90
QY	58	--YGAYDLDLGEFNQKGTVRTKY	TRNQIAQAVTSLKXNGIOVYGDVVMNHKGADGTE	115
DB	91	SKSGGEGYFWHDFKNG----	RYGSDAQLRQAASALGGAGVKLYDVVFNH-----	138
QY	116	IVNAVEVNRNRNQETSGEYAI	BAWTKFDPGGRGNHSSFKRWYHFDGTDWQSRQLQN	175
DB	139	-----MNRGYDPKEINLPAGQGF	W-RNDCADPGN-----YFNDCCDDGD-----	175
QY	176	KYKFRGTGKAWDWEVDTE	TENGYDILMYADVDMHDPEVIHELNRWGVYTTNTLNL-----	230
DB	176	---RFIG-----	GD-----ADLNTGHPQV-----YGMFRDEFNLRQYQ	207
QY	231	-DGRIDAVKHKIKYSTRDL	WLTHTVRNTTGPMPFAVAFWKNIDLGAI-----NYLNKTSWN	285
DB	208	AGGFREFVRGYAPERVNSWMT	DSADNS----FCVGLWK---GPSEYPNWDWRNTASWQ	260
QY	286	H-----	SVDVPLHNLYNASNGGYDMRNILNGSVVQKHPHATVTFVNDHDS	334
DB	261	QIIKWSDRACKCFVDFALKER	MON----GSIADWKHGLNGNDPRRREAVATVFDVNDHT	316
QY	335	--QPGF-----	AL--ESFVQWFKPLAYALVLTREQGYPSVF-----YGDYVGIP	376
DB	317	GYSPPQNGQGHWALQDGLIRQ	-----AYAILT-SFGTPVVTWNSHMYDWGYGDF-----	365
QY	377	HGVPAKMSKIDPLLQARQTF	FAYGTQHDYFDHHDIIIGWTREGNSHPNSGLATIMSDPGG	436
DB	366	-----IRQLIQVRR--	AAGVRAD-----SALSFH--SGVSGUATVSGS	400
QY	437	NKWMYVVKNI-----	KAGQVWRDITGNRTGVTINADGWNFS-----VNGGSVSVW	482
DB	401	QOTLVVVALNSDLGNPGQV	-----ASGSFSEAVNASNGQVRVW	437

RESULT 12

AM3D_ORYSA	STANDARD;	PRT;	435 AA.
ID AM3D_ORYSA			
AC P27933;			
DT 01-AUG-1992 (Rel. 23, Created)			
DT 01-AUG-1992 (Rel. 23, Last sequence update)			
DT 15-MAR-2004 (Rel. 43, Last annotation update)			
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).			
GN AMY1.3 OR AMY3D.			
OS Oryza sativa (Rice).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC Ehrhartoideae; Oryzaceae; Oryza.			
OX NCBI_TaxID=4530;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=cv. Japonica M202; TISSUE=EtIolated leaf;			
RX MEDLINE=9108278; PubMed=2263460;			
RA Huang N., Koizumi N., Reinl S., Rodriguez R.L.;			
RT "Structural organization and differential expression of rice alpha-			


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DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW Transferase; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT ACT_SITE 256 286 BY SIMILARITY.
FT ACT_SITE 284 284 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT METAL 54 54 CALCIUM 1 (BY SIMILARITY).
FT METAL 56 56 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 59 59 CALCIUM 1 (BY SIMILARITY).
FT METAL 60 60 CALCIUM 1 (BY SIMILARITY).
FT METAL 80 80 CALCIUM 1 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 2 (BY SIMILARITY).
FT METAL 217 217 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 226 226 CALCIUM 2 (BY SIMILARITY).
FT METAL 260 260 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 260 260 SIMILARITY).
SQ SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;

Query Match 9.9%; Score 269; DB 1; Length 713;
Best Local Similarity 22.1%; Pred. No. 5.2e-11;
Matches 114; Conservative 77; Mismatches 195; Indels 130; Gaps 23;

QY 21 GNHW-----NRLRDAANLKSQITAVWIPPAWKG-----TSQNDVGVGAYDYLDFGEF 69
DB 78 GGDWQGLINKND--GVLTGCVGTALWISQPVNIYSIYSGVNTVAHYGWARDFPKT 135

QY 70 NQKGTVRTKYGRNQLQAAVTSLSKNGIQYGVDMVNMHKGAGDGTETVNAVEVNRNRNQ 129
DB 136 N-----PAYGTTADFNQLIAAAHAKNIKVIIDFAPNHTSPASSDQ-PSFAENGRLVDNG 188

QY 130 ETSGEVAIEAWTKDFPGRGNHSSFKWRVHFDGTDWDSQRLQNKIYKRGTKANDW 189
DB 189 TLLGGVTNDTQNLF-----HHNGGTDFS----- 211

QY 190 EVDTEGNTDYLMADVDMDDHPEVIHE-----LRWGVWYWTNLDGFRIDAVKHKY 243
DB 212 --TTENGIIYKNL--YDLADLNHNSTSDVYLKDAIKMW-----LDLGDIDGIRMDAVKHMPF 263

QY 244 SFTRDWLTHVRNTGKPMFAVABFW--KNDLGAIEYLNKTSWNHVSFVDFPLHYNLYNA- 300
DB 264 GWQKSFMAAVNNY--KPVFTFGWFLGVNEVGP-ENHKFANESGMSLLDFRPAQKVRQVF 320

QY 301 -SNSGGYDMRNILNGSVQ-KHPTIAVTVDNHDSPGSALESFVQWFKPLAYALVLT 358
DB 321 RDNTDNMYGLKAMLEGSAAQVQDQVTFIDNHDMEFHASNANRRKLEQALAFLLIA 380

QY 359 REGQYSVFGV-DYV-----GIPTHGVPA-----MKSXIDPLQARQTFAYGTOH 402
DB 381 R---VPAIYVGTQYMSGGTDPDNRAKIPFSFTTAYQVIQKLPKRNPAIAYGSTQ 437

QY 403 DYFDHDDIIGWTREG-----NSSHPNSGLATIMSDGPGGNKMWYVYVGNKAKGQ 449
DB 438 ERWINDVLYERKFGSNVAVAVNRNLNAPASISGLVTSLPQGS----- 482

QY 450 VWDITGN--RTGVTVTINADG-WGNFVNGSGSVSW 482
DB 483 -YNDVLGGLLNGNTLVGSGGAASNFTLAAGGTAVW 517

RESULT 14
CDGT_BACSO
ID -CDGT_BACSO
AC P05618;
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FT	DOMAIN	523	609	D.	FT	STRAND	348	349
FT	DOMAIN	610	713	E.	FT	TURN	354	355
FT	ACT SITE	256	256		FT	TURN	362	363
FT	ACT SITE	284	284		FT	HELIX	366	378
FT	ACT SITE	355	355		FT	STRAND	382	386
FT	METAL	54	54		FT	TURN	387	388
FT	METAL	56	56	CALCIUM 1. (VIA CARBONYL OXYGEN).	FT	TURN	389	391
FT	METAL	59	59	CALCIUM 1.	FT	HELIX	392	392
FT	METAL	60	60	CALCIUM 1.	FT	TURN	398	399
FT	METAL	80	80	CALCIUM 1.	FT	TURN	400	402
FT	METAL	166	166	CALCIUM 2.	FT	HELIX	413	421
FT	METAL	217	217	CALCIUM 2. (VIA CARBONYL OXYGEN).	FT	TURN	422	423
FT	METAL	226	226	CALCIUM 2.	FT	HELIX	424	427
FT	METAL	260	260	CALCIUM 2. (VIA CARBONYL OXYGEN).	FT	HELIX	429	433
FT	DISULFID	70	77		FT	STRAND	435	441
FT	TURN	30	31		FT	STRAND	445	452
FT	TURN	33	34		FT	TURN	453	454
FT	TURN	40	41		FT	STRAND	455	462
FT	STRAND	44	46		FT	STRAND	469	471
FT	HELIX	49	51		FT	STRAND	475	475
FT	TURN	52	52		FT	STRAND	481	483
FT	HELIX	57	59		FT	TURN	486	491
FT	HELIX	63	65		FT	STRAND	496	498
FT	STRAND	66	66		FT	STRAND	500	502
FT	TURN	68	69		FT	HELIX	503	504
FT	TURN	73	74		FT	STRAND	507	509
FT	STRAND	76	76		FT	STRAND	511	512
FT	HELIX	81	89		FT	STRAND	514	519
FT	TURN	90	93		FT	STRAND	527	532
FT	HELIX	94	96		FT	STRAND	535	536
FT	TURN	97	97		FT	TURN	538	539
FT	STRAND	100	103		FT	STRAND	541	547
FT	STRAND	107	109		FT	STRAND	555	558
FT	STRAND	114	116		FT	TURN	559	560
FT	TURN	117	118		FT	STRAND	561	563
FT	STRAND	119	121		FT	HELIX	565	567
FT	TURN	124	125		FT	STRAND	568	571
FT	STRAND	129	135		FT	STRAND	575	579
FT	TURN	137	139		FT	STRAND	586	593
FT	HELIX	142	154		FT	TURN	595	596
FT	TURN	155	156		FT	STRAND	599	599
FT	STRAND	158	163		FT	STRAND	603	608
FT	TURN	165	166		FT	STRAND	613	621
FT	STRAND	167	170		FT	TURN	627	628
FT	TURN	176	177		FT	STRAND	630	635
FT	TURN	179	182		FT	HELIX	638	640
FT	STRAND	184	186		FT	TURN	641	643
FT	TURN	187	188		FT	HELIX	645	647
FT	STRAND	189	192		FT	STRAND	649	649
FT	TURN	195	196		FT	STRAND	653	653
FT	TURN	198	199		FT	TURN	660	661
FT	STRAND	202	202		FT	STRAND	663	670
FT	STRAND	207	207					
FT	HELIX	213	218					
FT	STRAND	220	220					
FT	TURN	222	223					
FT	STRAND	224	227					
FT	TURN	229	230					
FT	HELIX	232	247					
FT	TURN	248	249					
FT	STRAND	252	255					
FT	TURN	256	257					
FT	HELIX	258	260					
FT	HELIX	263	276					
FT	STRAND	280	283					
FT	TURN	289	290					
FT	HELIX	294	302					
FT	STRAND	306	308					
FT	HELIX	310	320					
FT	TURN	321	322					
FT	HELIX	327	340					
FT	TURN	342	343					
FT	HELIX	344	346					

Query Match 9.9%, Score 268; DB 1; Length 713;
Best Local Similarity 22.2%; Pred. No. 6.1e-11;
Matches 113; Conservative 81; Mismatches 200; Indels 114; Gaps 23;

Qy	21	GNHW-----NLRDDAANLKSKGITAVMIPPAWKG-----TSQNDVGYGAYDLYDLGEF	69
Db	78	GGDMOGIINKIND--GYLTGMITAIWISQVENIYSVINYGVNNTAYHGYWARDFKCT	135
Qy	70	NQKGTVRTKYTRNQLQAAVTSKKNNGIQVYGVYVMNHKGADGTEIVNAVEVNSNRNQ	129
Db	136	N-----PAYGTMQDFKNLIDTAHAHNIKVIIDFAPNHTSPASSDD-PSFAENGLYDNG	188
Qy	130	ETSGEYAIETWKTFDFPGRGNHSSFKRWYHFGTDQDSRQLQNKIYKFRGTGKAWDW	189
Db	189	NLLGGYTNDTQNLF-----HHYGTDFG-----TIENGIYK-----NLYDL	224
Qy	190	-EVDTEGNGVDYLMYADVMDHPEVIHELNRWGWYTYTNLNDGFRIDAVKHICYSTRD	248
Db	225	ADLNHNSSVDVYLKDAIKM-----WL--DLGVGDGIRVDVAKHMPFGWQKS	268

Qy	385	-----KIDPLQARQTF-----YGT-----QHDYFDHDIIGWTRGNSSHP	422
Db	418	TTTAFKEVSTLAGLRNNAAIQYGTQORWINNDVYIERKFFNDVVLVAINRNTQSSYS	477
Qy	423	NSGLATIMSDGP-----GGN-----KMMYVGKVKAGQVW--	451
Db	478	ISGLQALPNGSYADYLSGLLGGNGISVNSGVSASFLLAPGAVSVWQYSTSASAPQIGSV	537
Qy	452	---RDI TGNRTGTVTINADGWNF--SYNGGSVSVWVK	484
Db	538	APNMGIPGN---VVTIDKGFGTTQGTVTFGGVTATVK	572

Search completed: October 7, 2004, 00:13:16
Job time : 10.5063 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-2
Perfect score: 2714
Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGNGNFSVNGSVVWVKQ 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2714	100.0	485	2 AAW31499	AAW31499 Bacillus
2	2714	100.0	485	2 AAW48260	AAW48260 Bacillus
3	2714	100.0	485	2 AAY15421	AAY15421 Termamyl-
4	2714	100.0	485	2 AAY15415	AAY15415 Bacillus
5	2714	100.0	485	2 AAY25150	AAY25150 Bacillus
6	2714	100.0	485	2 AAY07391	AAY07391 Wild type
7	2714	100.0	485	2 AAY07381	AAY07381 Wild type
8	2714	100.0	485	3 AAY99602	AAY99602 Bacillus
9	2714	100.0	485	3 AAY99608	AAY99608 Bacillus
10	2714	100.0	485	5 ABB06933	ABB06933 Bacillus
11	2714	100.0	485	5 AAU12149	AAU12149 Bacillus
12	2714	100.0	485	5 AAB47850	AAB47850 Bacillus
13	2714	100.0	485	5 ABB76586	ABB76586 Termamyl-
14	2714	100.0	485	6 ABB99480	ABB99480 Amino aci
15	2712	99.9	485	2 AAW12113	AAW12113 Alpha-amy
16	2711	99.9	485	2 AAW12121	AAW12121 Alpha-amy
17	2711	99.9	485	2 AAW12099	AAW12099 Alpha-amy
18	2711	99.9	485	2 AAW12130	AAW12130 Alpha-amy
19	2711	99.9	485	2 AAW12107	AAW12107 Alpha-amy
20	2711	99.9	485	2 AAW12119	AAW12119 Alpha-amy
21	2711	99.9	485	2 AAW12102	AAW12102 Alpha-amy
22	2711	99.9	485	2 AAW12108	AAW12108 Alpha-amy
23	2711	99.9	485	2 AAW12106	AAW12106 Alpha-amy
24	2711	99.9	485	2 AAW12129	AAW12129 Alpha-amy
25	2711	99.9	485	2 AAW12118	AAW12118 Alpha-amy

26	2711	99.9	485	2 AAW12098	AAW12098 Alpha-amy
27	2711	99.9	485	2 AAW12103	AAW12103 Alpha-amy
28	2711	99.9	485	2 AAW12104	AAW12104 Alpha-amy
29	2711	99.9	485	2 AAW12105	AAW12105 Alpha-amy
30	2711	99.9	485	2 AAW12120	AAW12120 Alpha-amy
31	2711	99.9	485	2 AAW12100	AAW12100 Alpha-amy
32	2710	99.9	485	2 AAW12117	AAW12117 Alpha-amy
33	2709	99.8	485	2 AAW12122	AAW12122 Alpha-amy
34	2709	99.8	485	2 AAW12114	AAW12114 Alpha-amy
35	2709	99.8	485	2 AAW12125	AAW12125 Alpha-amy
36	2709	99.8	485	2 AAW12124	AAW12124 Alpha-amy
37	2709	99.8	485	2 AAW12123	AAW12123 Alpha-amy
38	2709	99.8	485	2 AAW12126	AAW12126 Alpha-amy
39	2709	99.8	485	2 AAW12131	AAW12131 Alpha-amy
40	2709	99.8	485	2 AAW12127	AAW12127 Alpha-amy
41	2709	99.8	485	2 AAW12128	AAW12128 Alpha-amy
42	2708	99.8	485	2 AAW12101	AAW12101 Alpha-amy
43	2708	99.8	485	2 AAW12112	AAW12112 Alpha-amy
44	2708	99.8	485	2 AAW12111	AAW12111 Alpha-amy
45	2707	99.7	485	2 AAW12144	AAW12144 Alpha-amy

ALIGNMENTS

RESULT 1
AAW31499
ID AAW31499 standard; protein; 485 AA.
AC AAW31499;
XX
DT 08-APR-1998 (first entry)
XX
DE Bacillus sp. alpha amylase.
XX
KW Alpha amylase; hard surface cleaning; dishwashing; laundry.
XX
OS Bacillus sp.
XX
PN W09732961-A2.
FD 12-SEP-1997.
XX
PF 04-MAR-1997; 97WO-US003635.
XX
PR 07-MAR-1996; 96WO-US003276.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;
XX Ward G;
XX WPI; 1997-457524/42.
XX
PT Detergent compositions for hard surface cleaning and laundry use -
XX contains Bacillus derived alpha amylase with improved thermostability;
XX reduced calcium ion dependency etc.
XX
PS Claim 1; Page 86-87; 97pp; English.
XX
CC The present sequence is a Bacillus sp. alpha amylase with a specific
XX activity at least 25% higher than that of Termamyl (RTM) at 25 to 55
XX degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It
XX is of use in hard surface cleaning, hand or machine dishwashing and
XX laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain
XX removal and fabric care are obtained by using it at a concentration of
XX 0.00018 to 0.06%
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.1e-206;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC	boosting fabric laundry performance or for dingy fabric cleanup			
XX				
SQ	Sequence 485 AA;			
	Query Match	100.0%;	Score 2714;	DB 2; Length 485;
	Best Local Similarity	100.0%;	Pred. No. 1.1e-206;	
	Matches 485;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA	60	
Db	1	HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA	60	
QY	61	YDLVDLGEFNGKGTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEIYNAV	120	
Db	61	YDLVDLGEFNGKGTVRTKYGTRNQLQAAVTSLKNGIQVYGDVVMNHKGGADGTEIYNAV	120	
QY	121	EVNRSNRNQETSGEYAEAWTKFDPGGRGNHSSFKRWYHFDGTDQDQSRQLQNKIYKF	180	
Db	121	EVNRSNRNQETSGEYAEAWTKFDPGGRGNHSSFKRWYHFDGTDQDQSRQLQNKIYKF	180	
QY	181	RGTKAWDEVDTEGNGYDLYMADVMDHPEVIHELNRWGVWYTTNLNLDGFRIDAVKH	240	
Db	181	RGTKAWDEVDTEGNGYDLYMADVMDHPEVIHELNRWGVWYTTNLNLDGFRIDAVKH	240	
QY	241	IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHSHVFDVPLHYNLYNA	300	
Db	241	IKYSFTRDMLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHSHVFDVPLHYNLYNA	300	
QY	301	SNSSGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQQWFKPLAYALVLTRE	360	
Db	301	SNSSGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQQWFKPLAYALVLTRE	360	
QY	361	QGYPSVFGDYGIPTGHPVAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS	420	
Db	361	QGYPSVFGDYGIPTGHPVAMKSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS	420	
QY	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFVSNGGSVS	480	
Db	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFVSNGGSVS	480	
QY	481	VWVKQ 485		
Db	481	VWVKQ 485		
RESULT 3				
AAV15421	AAV15421 standard; protein; 485 AA.			
ID	AAV15421;			
XX				
AC				
XX				
DT	22-JUL-1999 (first entry)			
XX				
DE	Termamyl-like alpha-amylase protein.			
XX				
KW	Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;			
XX				
KW	sweetener; ethanol; starch; textile desizing; starch liquefaction;			
XX				
OS	Bacillus sp.			
XX				
PN	WO9923211-A1.			
XX				
PD	14-MAY-1999.			
XX				
PF	30-OCT-1998; 98WO-DK000471.			
XX				
PR	30-OCT-1997; 97DK-00001240.			
XX				
PR	14-JUL-1998; 98DK-00000936.			
XX				
PA	(NOVO) NOVO-NORDISK AS.			
XX				
PI	Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;			

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PI Kjaerulff S;
XX
DR WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
XX
XX Claim 38; Page 88-89; 115pp; English.
XX
CC The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, M457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
XX
XX Sequence 485 AA;
XX
Query Match 100.0%; Score 2714; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.1e-206;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVMIPPAWKGTQNDVGGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVMIPPAWKGTQNDVGGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVVMMHKGADGTEIVNAV 120
DB 61 YDLYDLGEFNQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVVMMHKGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKRWYHFDGTDWQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKRWYHFDGTDWQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTEGNGYDLYMTADVMDHPEVIHELNNWGVWYTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTEGNGYDLYMTADVMDHPEVIHELNNWGVWYTNLTLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTCKPFAVEFKNKDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTCKPFAVEFKNKDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
DB 301 SNSGGYYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMSKIDPLQARQTFAYGQTHDYFDHHDIIIGWTREGNSS 420
DB 361 QGYPSVFGDYGIPTHGVPAMSKIDPLQARQTFAYGQTHDYFDHHDIIIGWTREGNSS 420
QY 421 HPNSGLATIMSDPGGKNMVMYGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDPGGKNMVMYGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 VWYKQ 485
DB 481 VWYKQ 485

RESULT 4
ID AAY15415
XX AAY15415 standard; protein; 485 AA.
XX
AC AAY15415;
XX
DT 22-JUL-1999 (first entry)
XX

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DE Bacillus strain NCIB 12512 alpha-amylase protein.
XX
XX Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
XX sweetener; ethanol; starch; textile desizing; starch liquefaction;
XX saccharification process.
XX
XX Bacillus sp.
XX
XX WO9923211-A1.
XX
XX 14-MAY-1999.
XX
XX 30-OCT-1998; 98WO-DK000471.
XX
XX 30-OCT-1997; 97DK-00001240.
XX
XX 14-JUL-1998; 98DK-00000936.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
XX Kjaerulff S;
XX
XX WPI; 1999-326987/27.
XX
XX New Termamyl-like alpha-amylase variants.
XX
XX Claim 38; Page 77-79; 115pp; English.
XX
CC The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
CC K311, E346, K385, G456, M457, K458, P459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
XX
XX Sequence 485 AA;
XX
Query Match 100.0%; Score 2714; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.1e-206;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVMIPPAWKGTQNDVGGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVMIPPAWKGTQNDVGGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVVMMHKGADGTEIVNAV 120
DB 61 YDLYDLGEFNQKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVVMMHKGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKRWYHFDGTDWQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYAEAWTKFDFPGRGNHNSFKRWYHFDGTDWQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTEGNGYDLYMTADVMDHPEVIHELNNWGVWYTNLTLDGFRIDAVKH 240
DB 181 RGTGKAWDEVDTEGNGYDLYMTADVMDHPEVIHELNNWGVWYTNLTLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTCKPFAVEFKNKDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNTTCKPFAVEFKNKDLGAIENYLNKTSWNHNSVFDVPLHYNLYNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
DB 301 SNSGGYYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGIPTHGVPAMSKIDPLQARQTFAYGQTHDYFDHHDIIIGWTREGNSS 420

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Db 361 QGYPSVFGYGGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDIIGWTREGNS 420
 QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
 Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
 QY 481 VVVKQ 485
 Db 481 VVVKQ 485
 RESULT 5
 AAY25150
 ID AAY25150 standard; protein; 485 AA.
 AC AAY25150;
 XX 27-AUG-1999 (first entry)
 DT Bacillus sp. alpha-amylase protein fragment 1.
 DE Alpha-amylase; cleaning composition; protease variant; spot removal;
 KW detergent composition; hard surface cleaning; fabric cleaning;
 KW dishwashing composition; oral cleaning composition; personal cleansing;
 KW stain removal; soil removal; whiteness maintenance; dingy cleanup;
 KW film removal.
 XX
 OS Bacillus sp.
 XX WO9920723-A2.
 PN 29-APR-1999.
 XX 23-OCT-1998; 98WO-US022486.
 PF 23-OCT-1997; 97US-00956323.
 PR 23-OCT-1997; 97US-00956324.
 PR 23-OCT-1997; 97US-00956564.
 XX (PROC) PROCTER & GAMBLE CO.
 PA Ghosh CK, Baek AC, Ohtani R, Busch A, Showell MS;
 XX WPI; 1999-404706/34.
 XX Cleaning compositions used in e.g. detergent for cleaning hard surfaces
 PT or fabrics, dishwashing or oral cleaning comprises protease and amylase
 PT variants having amino acid residues.
 XX Claim 1b(ii); Page 164-165; 169pp; English.
 XX This invention describes novel cleaning compositions which contain a
 CC protease variant with an amino acid substitution corresponding to
 CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.
 CC The compositions can be used in e.g. detergent compositions, for cleaning
 CC hard surfaces or fabrics, dishwashing compositions, oral cleaning
 CC compositions, detergent cleaning compositions and personal cleaning
 CC compositions. The combination of protease variants and alpha-amylase
 CC variants in cleaning compositions can provide improved and enhanced
 CC cleaning ability, including stain and/or soil removal and/or reduction
 CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or film
 CC removal and/or reduction, over conventional enzyme-containing cleaning
 CC compositions
 XX Sequence 485 AA;
 SQ Query Match 100.0%; Score 2714; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HNGTNGTMMQYFEWYLPNDGNHNLRLDAAKLSKGTAVWIPPAWKTSQNDVGYGA 60
 |||||

Db 1 HNGTNGTMMQYFEWYLPNDGNHNLRLDAAKLSKGTAVWIPPAWKTSQNDVGYGA 60
 QY 61 YLDYDLGEFNQKGTATKTKYTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 |||||
 Db 61 YLDYDLGEFNQKGTATKTKYTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 |||||
 QY 121 EVNRSNRNQETSCEYAIEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
 Db 121 EVNRSNRNQETSCEYAIEAWTKFDFPGRGNHNSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
 |||||
 QY 181 RGTGKAWDEVDTEGNGYDYLKAYADYMDHPPEVIHELNRWGVWYTTNLNDGFRIDAVKH 240
 Db 181 RGTGKAWDEVDTEGNGYDYLKAYADYMDHPPEVIHELNRWGVWYTTNLNDGFRIDAVKH 240
 |||||
 QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAENYLNKTSWNHSVFDVPLHYNLNA 300
 Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFKNDLGAENYLNKTSWNHSVFDVPLHYNLNA 300
 |||||
 QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALSFVQWFKPLAYALVLTRE 360
 Db 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALSFVQWFKPLAYALVLTRE 360
 |||||
 QY 361 QGYPSVFGYGGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDIIGWTREGNS 420
 Db 361 QGYPSVFGYGGIPTHGVPAKSKIDPLQARQTFAYGTQHDYFDHDIIGWTREGNS 420
 |||||
 QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
 Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGSGVS 480
 |||||
 QY 481 VVVKQ 485
 Db 481 VVVKQ 485
 RESULT 6
 AAY07391
 ID AAY07391 standard; protein; 485 AA.
 AC AAY07391;
 XX 16-JUL-1999 (first entry)
 DT Wild type Termamyl(RTM)-like alpha-amylase protein #7.
 DE Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
 XX dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
 KW ethanol.
 XX Bacillus sp.
 OS WO9919467-A1.
 PN 22-APR-1999.
 PD 13-OCT-1998; 98WO-DK000444.
 PF 13-OCT-1997; 97DK-00001172.
 PR (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Borchert TV, Bisgard-Frantzen H;
 PI WPI; 1999-277632/23.
 DR Variant alpha-amylases - useful as detergents or for textile desizing or
 PT starch liquefaction.
 PT Disclosure; Page 72-74; 93pp; English.
 PS This sequence represents the parent sequence for new variants of a parent
 CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase

CC from either of two Bacillus species in W09526397, B. stearothermophilus,
 CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
 CC amylase variants are detergent additives for use in detergents for
 CC dishwashing, manual or automatic laundry. The variants can also be used
 CC for textile desizing or starch liquefaction (e.g. for production of
 CC sweeteners or ethanol)
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60
 Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGFEFNQKGTVRTKYGRNQLAAVTSKNGIQVYGVVNMHKGADGTEIVNAV 120
 Db 61 YDLYDLGFEFNQKGTVRTKYGRNQLAAVTSKNGIQVYGVVNMHKGADGTEIVNAV 120

Qy 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHNSFKRWYHFDGTDQSRQLQNKLYKF 180
 Db 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHNSFKRWYHFDGTDQSRQLQNKLYKF 180

Qy 181 RGTGKAWDWEVDTEGNYDYLMYADVMDHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240
 Db 181 RGTGKAWDWEVDTEGNYDYLMYADVMDHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240

Qy 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFKNDLGAENYLNKTSWNHSHVDFVPLHYNLYNA 300
 Db 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFKNDLGAENYLNKTSWNHSHVDFVPLHYNLYNA 300

Qy 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQOQFKPLAYALVLTRE 360
 Db 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQOQFKPLAYALVLTRE 360

Qy 361 QGYPVSFYGDYGIPTHTGVPAKSKIDPLQARQTFAYGTOHDFDHHDIIGWTRGNS 420
 Db 361 QGYPVSFYGDYGIPTHTGVPAKSKIDPLQARQTFAYGTOHDFDHHDIIGWTRGNS 420

Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTITNADGWGNSVNGGSVS 480
 Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTITNADGWGNSVNGGSVS 480

Qy 481 VVVKQ 485
 Db 481 VVVKQ 485

RESULT 7

AAAY07381
 ID AAAY07381 standard; protein; 485 AA.
 XX AC
 XX AAAY07381;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Wild type Termamyl (RTM)-like alpha-amylase protein #1.
 XX
 KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
 KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
 KW ethanol.
 XX
 OS Bacillus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 181..184
 FT /note= "optionally 1, 2, 3 or all residues are deleted"
 FT Misc-difference 195
 FT /note= "optionally altered to any amino acid except an
 FT Asn residue"
 FT Misc-difference 206

FT /note= "optionally altered to any amino acid except a Val
 residue"
 FT Misc-difference 212
 FT /note= "optionally altered to any amino acid except a Glu
 residue"
 FT Misc-difference 216
 FT /note= "optionally altered to any amino acid except a Glu
 residue"
 FT Misc-difference 269
 FT /note= "optionally altered to any amino acid except a Lys
 residue"
 XX
 XX W09919467-A1.
 XX 22-APR-1999.
 XX 13-OCT-1998; 98WO-DK000444.
 XX 13-OCT-1997; 97DK-00001172.
 XX (NOVO) NOVO-NORDISK AS.
 XX Svendsen A, Borchert TV, Bisgaard-Frantzen H;
 XX WPI; 1999-277632/23.
 XX Variant alpha-amylases - useful as detergents or for textile desizing or
 starch liquefaction.
 XX Claim 1; Page 61-63; 93pp; English.
 PS This sequence represents the parent sequence for new variants of a parent
 CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
 CC from either of two Bacillus species in W09526397, B. stearothermophilus,
 CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
 CC amylase variants are detergent additives for use in detergents for
 CC dishwashing, manual or automatic laundry. The variants can also be used
 CC for textile desizing or starch liquefaction (e.g. for production of
 CC sweeteners or ethanol)
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60
 Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGFEFNQKGTVRTKYGRNQLAAVTSKNGIQVYGVVNMHKGADGTEIVNAV 120
 Db 61 YDLYDLGFEFNQKGTVRTKYGRNQLAAVTSKNGIQVYGVVNMHKGADGTEIVNAV 120

Qy 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHNSFKRWYHFDGTDQSRQLQNKLYKF 180
 Db 121 EVNRSNRNQETSGEYATEAWTKFDPGRGNHNSFKRWYHFDGTDQSRQLQNKLYKF 180

Qy 181 RGTGKAWDWEVDTEGNYDYLMYADVMDHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240
 Db 181 RGTGKAWDWEVDTEGNYDYLMYADVMDHPEVHELNRNGVWYTNLTLDGFRIDAVKH 240

Qy 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFKNDLGAENYLNKTSWNHSHVDFVPLHYNLYNA 300
 Db 241 IKYSFTRDMLTHVRNTTCKPMFAVAEFKNDLGAENYLNKTSWNHSHVDFVPLHYNLYNA 300

Qy 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQOQFKPLAYALVLTRE 360
 Db 301 SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQOQFKPLAYALVLTRE 360

Qy 361 QGYPVSFYGDYGIPTHTGVPAKSKIDPLQARQTFAYGTOHDFDHHDIIGWTRGNS 420
 Db 361 QGYPVSFYGDYGIPTHTGVPAKSKIDPLQARQTFAYGTOHDFDHHDIIGWTRGNS 420

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Db 361 QGYPSVFYGDYIGIPTHGVPAKSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 8
AA99602
ID AA99602 standard; protein; 485 AA.
XX
XX AA99602;
XX
DT 04-SBP-2000 (first entry)
XX
XX Bacillus parent Termamyl-like alpha-amylase #1.
XX
XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; mutein; mutant; enzyme stability; hybrid.
XX
XX Bacillus sp.
OS
XX WO200029560-A1.
XX
XX 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-DK000628.
XX
PR 16-NOV-1998; 98DK-00001495.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
XX
XX WPI; 2000-387777/33.
DR
DR N-PSDB; AAA48480.
XX
XX Variant of parent termamyl-like alpha amylase useful for washing, textile
PT desizing and starch liquefaction, comprising alterations in one or more
PT solvent exposed amino acid residues.
XX
XX Claim 8; Page 53-54; 80pp; English.
XX
XX The present sequence is a parent Termamyl-like alpha-amylase from which
CC mutants with increased stability at acidic pH, low calcium concentration
CC and high temperatures have been derived. The sequence encoding this
CC protein was isolated from a Bacillus genomic DNA library. A variant may
CC contain mutations in one or more solvent exposed amino acid residues to
CC increase the overall hydrophobicity of the enzyme or the overall number
CC of methyl groups in the side chains of exposed residues may be increased.
CC The mutations can be incorporated by site-directed mutagenesis or by
CC random mutagenesis. As a result of their increased stability, the
CC variants are suitable for the industrial processing of starch, i.e.
CC starch liquefaction and saccharification. They may also be useful for
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
CC comprising partial amino acid sequences derived from two or more alpha-
CC amylases have also been created in order to increase enzyme stability
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.1e-206;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTQNDVGYGA 60
Db 1 HNGTGTMMQYFEWYLPNDGNHNRRLDDAANKSKGITAVWIPPAWKGTQNDVGYGA 60
QY 61 YDYLDFGEFNQKGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120

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Db 61 YDYLDFGEFNQKGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQBTSGEYAI EAWTKFDFPGRGNHSHSFKWRWYHFDGTQDWDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQBTSGEYAI EAWTKFDFPGRGNHSHSFKWRWYHFDGTQDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDEVDTPENGNYDYLMTYADVMDHPHPEVIHEL RNKGWVWYTNLTNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTPENGNYDYLMTYADVMDHPHPEVIHEL RNKGWVWYTNLTNDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHTVRNTTGKPMFAVAFKNDLGA IENYLNKTSWNHSHSVFDPVPLHYNLYNA 300
Db 241 IKYSFTRDMLTHTVRNTTGKPMFAVAFKNDLGA IENYLNKTSWNHSHSVFDPVPLHYNLYNA 300
QY 301 SMSGYYDMENILNGSVVQKHPTHAVTFVDNHDHSDQGEALSFVQWKFELAYALVLTRE 360
Db 301 SMSGYYDMENILNGSVVQKHPTHAVTFVDNHDHSDQGEALSFVQWKFELAYALVLTRE 360
QY 361 QGYPSVFYGDYIGIPTHGVPAKSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
Db 361 QGYPSVFYGDYIGIPTHGVPAKSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 9
AA99608
ID AA99608 standard; protein; 485 AA.
XX
XX AA99608;
XX
DT 04-SBP-2000 (first entry)
XX
XX Bacillus Termamyl-like alpha-amylase.
XX
XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; mutein; mutant; enzyme stability; hybrid.
XX
XX Bacillus sp.
OS
XX WO200029560-A1.
XX
XX 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-DK000628.
XX
PR 16-NOV-1998; 98DK-00001495.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
XX
XX WPI; 2000-387777/33.
PT
PT Variant of parent termamyl-like alpha amylase useful for washing, textile
PT desizing and starch liquefaction, comprising alterations in one or more
PT solvent exposed amino acid residues.
XX
XX Claim 8; Page 62-64; 80pp; English.
XX
XX The present sequence is a parent alpha-amylase from which mutants with
CC increased stability at acidic pH, low calcium concentration and high
CC temperatures have been derived. The sequence encoding this enzyme was
CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of methyl

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CC groups in the side chains of exposed residues may be increased. The
 CC mutations can be incorporated by site-directed mutagenesis or by random
 CC mutagenesis. As a result of their increased stability, the variants are
 CC suitable for the industrial processing of starch, i.e. starch
 CC liquefaction and saccharification. They may also be useful for washing,
 CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
 CC partial amino acid sequences derived from two or more alpha-amylases have
 CC also been created in order to increase enzyme stability

XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 3; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTNGTMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVWIPPAWKGTQNDVGGA 60
 DB 1 HHNGTNGTMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVWIPPAWKGTQNDVGGA 60

QY 61 YDLVGLGEFNQKGVTRTKYGTNRNQLAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 DB 61 YDLVGLGEFNQKGVTRTKYGTNRNQLAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120

QY 121 EVNRSNRNQTSGEYATIAEAWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
 DB 121 EVNRSNRNQTSGEYATIAEAWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

QY 181 RGTGKAWDWEVDTENGNYDYLMDVDMDPHEVTHELRNKGWVYTNLTLDGFRIDAVKH 240
 DB 181 RGTGKAWDWEVDTENGNYDYLMDVDMDPHEVTHELRNKGWVYTNLTLDGFRIDAVKH 240

QY 241 IKYSFTRDWLTHVNTTGGKPMFAVAEFGKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300
 DB 241 IKYSFTRDWLTHVNTTGGKPMFAVAEFGKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300

QY 301 SNSSGYDDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
 DB 301 SNSSGYDDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360

QY 361 QGYPSPFYGYDYGIPTHGVPAKMSKIDPLQAROTFAYGTHQHDYFDHDDIIGWTREGNSS 420
 DB 361 QGYPSPFYGYDYGIPTHGVPAKMSKIDPLQAROTFAYGTHQHDYFDHDDIIGWTREGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFGNSVSGSVS 480
 DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFGNSVSGSVS 480

QY 481 VVVKQ 485
 DB 481 VVVKQ 485

RESULT 10

ABB06933
 ID ABB06933 standard; protein; 485 AA.
 XX AC ABB06933;
 XX DT 19-JUN-2002 (first entry)
 XX
 DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:2.
 XX
 KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX OS Bacillus sp.
 XX PN W0200166712-A2.
 XX PD 13-SEP-2001.
 XX PF 07-MAR-2001; 2001WO-DK000144.

XX 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX (NOVO) NOVOZYMES AS.

XX Andersen C, Borchert TV, Nielsen BR;

PI WPI; 2002-239612/29.

DR N-PSDB; ABL50564.

XX Novel variant of parent termamyl-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.

PS Claim 8; Page 132-133; 153pp; English.

XX The present invention describes a variant of a parent termamyl-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a Bacillus termamyl-like alpha-amylase which
 CC is used in the exemplification of the present invention

XX Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 5; Length 485;

Best Local Similarity 100.0%; Pred. No. 1.1e-206;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTNGTMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVWIPPAWKGTQNDVGGA 60
 DB 1 HHNGTNGTMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVWIPPAWKGTQNDVGGA 60

QY 61 YDLVGLGEFNQKGVTRTKYGTNRNQLAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 DB 61 YDLVGLGEFNQKGVTRTKYGTNRNQLAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120

QY 121 EVNRSNRNQTSGEYATIAEAWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
 DB 121 EVNRSNRNQTSGEYATIAEAWTKDFPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

QY 181 RGTGKAWDWEVDTENGNYDYLMDVDMDPHEVTHELRNKGWVYTNLTLDGFRIDAVKH 240
 DB 181 RGTGKAWDWEVDTENGNYDYLMDVDMDPHEVTHELRNKGWVYTNLTLDGFRIDAVKH 240

QY 241 IKYSFTRDWLTHVNTTGGKPMFAVAEFGKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300
 DB 241 IKYSFTRDWLTHVNTTGGKPMFAVAEFGKNDLGAENYLNKTSWNHVSFVDFPLHNLNA 300

QY 301 SNSSGYDDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360
 DB 301 SNSSGYDDMRNILNGSVVQKHPTHAVTFVDNHDSPQGEALSFVQWFKPLAYALVLTRE 360

QY 361 QGYPSPFYGYDYGIPTHGVPAKMSKIDPLQAROTFAYGTHQHDYFDHDDIIGWTREGNSS 420
 DB 361 QGYPSPFYGYDYGIPTHGVPAKMSKIDPLQAROTFAYGTHQHDYFDHDDIIGWTREGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFGNSVSGSVS 480
 DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFGNSVSGSVS 480

QY 481 VVVKQ 485

[illegible]

CC kda has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
 DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
 QY 61 YDLYDLGEFNGKQTVRTKYGTRNQLQAQVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 DB 61 YDLYDLGEFNGKQTVRTKYGTRNQLQAQVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 QY 121 EVNRSNRNQTSGEYAEAWTKFDPGGRNHNHSSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
 DB 121 EVNRSNRNQTSGEYAEAWTKFDPGGRNHNHSSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
 QY 181 RGTGKAWDEVDTEGNYDYLMDVDMHPEVTHELRNMGVWYTNLTNLDGFRIDAVKH 240
 DB 181 RGTGKAWDEVDTEGNYDYLMDVDMHPEVTHELRNMGVWYTNLTNLDGFRIDAVKH 240
 QY 241 IKYSFTRDLTHVNTTGGKPMFAVAEFWKNDLGAENYLNKTSNHSVDFVPLHYNLYNA 300
 DB 241 IKYSFTRDLTHVNTTGGKPMFAVAEFWKNDLGAENYLNKTSNHSVDFVPLHYNLYNA 300
 QY 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
 DB 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
 QY 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTHDYFDHDIIGWTREGNSS 420
 DB 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTHDYFDHDIIGWTREGNSS 420
 QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
 DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
 QY 481 VWVKQ 485
 DB 481 VWVKQ 485

RESULT 13
 ABB76586
 ID ABB76586 standard; protein; 485 AA.
 XX
 AC ABB76586;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Termamyl-like-alpha-amylase #1.
 XX
 KW Termamyl; alpha amylase; starch liquefaction; ethanol production;
 KW textile desizing; detergent; enzyme.
 XX
 OS Bacillus sp.
 XX
 PN WO200210355-A2.
 XX
 PD 07-FEB-2002.
 XX
 PP 12-JUL-2001; 2001WO-DK000488.

XX 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX (NOVO) NOVOZYMES AS.
 PA
 XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 PI
 XX WPI; 2002-280633/32.
 DR N-ESDB; ABL96207.
 XX
 PT Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 8; Fig 2; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyl-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120plusoc and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2714; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.1e-206;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
 DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA 60
 QY 61 YDLYDLGEFNGKQTVRTKYGTRNQLQAQVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 DB 61 YDLYDLGEFNGKQTVRTKYGTRNQLQAQVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
 QY 121 EVNRSNRNQTSGEYAEAWTKFDPGGRNHNHSSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
 DB 121 EVNRSNRNQTSGEYAEAWTKFDPGGRNHNHSSFKWRWYHFDGTDWDQSRQLQNKIYKF 180
 QY 181 RGTGKAWDEVDTEGNYDYLMDVDMHPEVTHELRNMGVWYTNLTNLDGFRIDAVKH 240
 DB 181 RGTGKAWDEVDTEGNYDYLMDVDMHPEVTHELRNMGVWYTNLTNLDGFRIDAVKH 240
 QY 241 IKYSFTRDLTHVNTTGGKPMFAVAEFWKNDLGAENYLNKTSNHSVDFVPLHYNLYNA 300
 DB 241 IKYSFTRDLTHVNTTGGKPMFAVAEFWKNDLGAENYLNKTSNHSVDFVPLHYNLYNA 300
 QY 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
 DB 301 SNSGGYDMRNILNGSVVQKHPHTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
 QY 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTHDYFDHDIIGWTREGNSS 420
 DB 361 QGTPSVFYGYIGIPTHGVPAKSKIDPLQARQTFAYGTHDYFDHDIIGWTREGNSS 420
 QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
 DB 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNFVSNGGSVS 480
 QY 481 VWVKQ 485
 DB 481 VWVKQ 485
 RESULT 14
 ABB99480
 ID ABB99480 standard; protein; 485 AA.
 XX

AC ABB99480;
 XX 12-FEB-2003 (first entry)
 XX Amino acid sequence of an alpha-amylase.
 DE Alpha-amylase; enzyme; detergent; boric acid.
 XX Alkaliphilic bacillus.
 XX WO200268575-A1.
 XX 06-SEP-2002.
 XX 25-FEB-2002; 2002WO-US005512.
 XX 28-FEB-2001; 2001US-00795211.
 XX (PROC) PROCTER & GAMBLE CO.
 XX Kasturi C, Wandrat ME, Song BX;
 XX WPI; 2003-058303/05.
 XX Aqueous liquid or gel type detergent, useful as automatic dishwashing
 PT composition, comprises boric acid or born compound, polyhydroxy compound,
 PT calcium ions and alpha-amylase enzyme.
 XX Claim 1; Page 22-25; 36pp; English.
 XX The present sequence represents an alpha-amylase. The enzyme is used in
 CC detergents of the invention. The specification describes an aqueous
 CC liquid or gel type detergent composition, which comprises boric acid or a
 CC boron compound capable of forming boric acid in the composition, a
 CC polyhydroxy compound, calcium ions and selected alpha-amylase enzyme. The
 CC detergent composition is useful for stabilizing an amylase enzyme in an
 CC aqueous liquid or gel type detergent composition. It is useful for
 CC cleaning tableware (e.g. glassware, china, silverware, plastics),
 CC kitchenware, household surface such as floors, bathroom fixtures and
 CC countertops, and fabrics. It is useful as a fully formulated cleaning
 CC powder or as an additive or specialty product that is used alone or with
 CC other cleaning products. It is particularly useful in automatic
 CC dishwashing machine
 XX Sequence 485 AA;
 SQ
 Query Match 100.0%; Score 2714; DB 6; Length 485;
 Best Local Similarity 100.0%; Pred. No. 1.le-206;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HNGTGTWQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSQNDVGYGA 60
 DB 1 HNGTGTWQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSQNDVGYGA 60
 QY YDLYDLGEFQKGTVRTKYTRNLQQAATVSLKNGIQVYGVVMMHKGADGTEIVNAV 120
 DB YDLYDLGEFQKGTVRTKYTRNLQQAATVSLKNGIQVYGVVMMHKGADGTEIVNAV 120
 QY EVNRNENQTSGEYATEAMTKDFPGRGNHNSFKWRVHFDGTWDQSRQLQNKIYKF 180
 DB EVNRNENQTSGEYATEAMTKDFPGRGNHNSFKWRVHFDGTWDQSRQLQNKIYKF 180
 QY RGTGKAWDWEVDTEGNYDLYMADVMDHPEVIELRNWGVWYTNLNDGFRIDAVKH 240
 DB RGTGKAWDWEVDTEGNYDLYMADVMDHPEVIELRNWGVWYTNLNDGFRIDAVKH 240
 QY IKYSFTRDMLTHVRNTGKPMFAVEAFWKNDLGAENLYNKTWNHNSVFDVPLHYNLYNA 300
 DB IKYSFTRDMLTHVRNTGKPMFAVEAFWKNDLGAENLYNKTWNHNSVFDVPLHYNLYNA 300
 QY SNSGGYYDMENILNGSVVQKHPHATVFDVNDHDSQPGEALESFVQWFKLAYALVITRE 360
 DB SNSGGYYDMENILNGSVVQKHPHATVFDVNDHDSQPGEALESFVQWFKLAYALVITRE 360

QY 361 QGYPSVFGDYGYGIPTHGVPAMKSKIDPLQARQTFAVGTQHDYFDHDIIGWTRGNS 420
 DB 361 QGYPSVFGDYGYGIPTHGVPAMKSKIDPLQARQTFAVGTQHDYFDHDIIGWTRGNS 420
 QY 421 HPNSGLATIMSDPGGNKMWYGVKNGKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
 DB 421 HPNSGLATIMSDPGGNKMWYGVKNGKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
 QY 481 VVVKQ 485
 DB 481 VVVKQ 485
 RESULT 15
 AAW12113
 ID AAW12113 standard; protein; 485 AA.
 XX AAW12113;
 AC AAW12113;
 XX 08-APR-1997 (first entry)
 DT DT
 XX Alpha-amylase variant L2171.
 DE Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
 XX calcium ion dependency; alpha-amylolytic activity; washing composition;
 KW textile desizing; papermaking; beer-making; ethanol production;
 KW sweetener.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 217
 FT /label= L2171
 XX WO9623873-A1.
 PN 08-AUG-1996.
 PD 05-FEB-1996; 96WO-DK000056.
 XX 03-FEB-1995; 95DK-00000126.
 PR 29-MAR-1995; 95DK-00000336.
 PR 29-SEP-1995; 95DK-00001097.
 PR 06-OCT-1995; 95DK-00001121.
 XX (NOVO) NOVO-NORDISK AS.
 PA Bisgard-Frantzen H, Svendsen A, Borchert T;
 XX WPI; 1996-371423/37.
 DR Alpha-amylase variants - with improved thermal and oxidation stability
 XX and reduced calcium ion dependency.
 PT Claim 10; Page ?; 111pp; English.
 PS
 XX AAW12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by AAW12095, AAW12096, AAW12097, AAW12098, AAW12099-
 CC W12136, AAW12141, AAW12142 and AAW12144 are specifically variants of the
 CC alkaliphilic Bacillus strain NCIB 12512 alpha-amylase shown in AAW12098.
 CC These variants can have improved thermal stability (such as at
 CC temperatures in the range of 40-70 degrees Celsius), and/or oxidation
 CC stability, and/or reduced calcium ion dependency. The variants can also
 CC have increased alpha-amylolytic activity (especially at pH values in the
 CC range of 8.5-10.5), and improved binding of a particular substrate. These
 CC variant alpha-amylases also possess improved specificity to a particular
 CC substrate, and/or improved specificity with respect to cleavage of
 CC substrate. These sequences can be used in detergent and washing
 CC compositions, and for textile desizing. The alpha-amylase variants can
 CC also be used in papermaking and beer-making processes. These variants can

CC also be used in the production of sweeteners and ethanol from starch

XX Sequence 485 AA;

Query Match 99.9%; Score 2712; DB 2; Length 485;
Best Local Similarity 99.8%; Pred. No. 1.6e-206;
Matches 484; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HHNGTNGTMQYF	WYLPNDGNHNRLRDDAANKSGKITAVIPPAWKTSQNDVG	YGA	60
Db	1	HHNGTNGTMQYF	WYLPNDGNHNRLRDDAANKSGKITAVIPPAWKTSQNDVG	YGA	60
Qy	61	YDLVDLGEFNQKGT	VRKYGTRNQLQAAVTSLKNGIQVYGDVVNMHKG	ADGTEI	120
Db	61	YDLVDLGEFNQKGT	VRKYGTRNQLQAAVTSLKNGIQVYGDVVNMHKG	ADGTEI	120
Qy	121	EVNRSNRNQETS	GEYAEAWTKFDPGGRGNHSHFKRWYHFDGTDWDQSRQLQ	KNKIYKF	180
Db	121	EVNRSNRNQETS	GEYAEAWTKFDPGGRGNHSHFKRWYHFDGTDWDQSRQLQ	KNKIYKF	180
Qy	181	RGTCKAMDWE	VDTEGNYDYLMYADVMDHPEVIHELNNGWVWYTNLT	NLDGFRIDAVKH	240
Db	181	RGTCKAMDWE	VDTEGNYDYLMYADVMDHPEVIHELNNGWVWYTNLT	NLDGFRIDAVKH	240
Qy	241	IKYSFTRDWL	THVRNTTGKPMFAVAEPWKNDLGAIENTYLNKTSWNH	SFVDPPLHYNLYNA	300
Db	241	IKYSFTRDWL	THVRNTTGKPMFAVAEPWKNDLGAIENTYLNKTSWNH	SFVDPPLHYNLYNA	300
Qy	301	SNSGGYDMRN	ILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQOWFKPLAYAL	VLVLTRE	360
Db	301	SNSGGYDMRN	ILNGSVVQKHPTAVTFVDNHDSPQGEALSFVQOWFKPLAYAL	VLVLTRE	360
Qy	361	QGYPSVFYGDY	YGIPTHGVPAMSKIDPLQARQTFAYGTOHDYFDHHDII	IGWTREGNSS	420
Db	361	QGYPSVFYGDY	YGIPTHGVPAMSKIDPLQARQTFAYGTOHDYFDHHDII	IGWTREGNSS	420
Qy	421	HPNSGLATIMS	DGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADG	WGNFVNGGSVS	480
Db	421	HPNSGLATIMS	DGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADG	WGNFVNGGSVS	480
Qy	481	VWKQ	485		
Db	481	VWKQ	485		

Search completed: October 7, 2004, 00:12:11
Job time : 62.5516 secs

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-2
Perfect score: 2714
Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGKGNFVNGSGSVVWKQ 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2440	89.9	518	1 A27705	alpha-amylase (EC
2	1909.5	70.4	549	1 A54541	alpha-amylase (EC
3	1905	70.2	512	1 ALBSL	alpha-amylase (EC
4	1898.5	70.0	549	1 A24549	alpha-amylase (EC
5	1892.5	69.7	549	1 A24436	alpha-amylase (EC
6	1850	68.2	514	1 ALBSN	alpha-amylase (EC
7	1831	67.5	548	1 ALBSF	alpha-amylase (EC
8	1344	49.5	493	2 S15713	alpha-amylase (EC
9	1245	45.9	484	2 G95160	alpha-amylase (imp
10	1243	45.8	484	2 F98026	alpha-amylase (EC
11	1239	45.7	492	2 AH2079	alpha-amylase (imp
12	1127	41.5	491	2 C86781	alpha-amylase (imp
13	1097	40.4	506	2 G98247	cytoplasmic alpha-
14	1096	40.4	495	2 AD3038	alpha-amylase (EC
15	1076	39.6	494	1 B45738	alpha-amylase (EC
16	1066	39.3	494	2 AD0751	cytoplasmic alpha-
17	1054	38.8	495	2 B90962	cytoplasmic alpha-
18	1049	38.7	495	1 A45738	alpha-amylase (EC
19	1035	38.1	495	2 B85810	cytoplasmic alpha-
20	382.5	14.1	217	2 AL9506	alpha-amylase (EC
21	316	11.6	1196	2 A29130	beta-amylase (EC 3
22	305.5	11.3	421	2 S10514	alpha-amylase (EC
23	295.5	10.9	482	2 S31478	alpha-amylase (EC
24	294	10.8	440	2 S14958	alpha-amylase (EC
25	289.5	10.7	551	2 S05667	glucan 1,4-alpha-m
26	288	10.6	423	2 T09942	alpha-amylase (EC
27	285.5	10.5	826	2 E96720	probable alpha-amy
28	274.5	10.1	547	2 A32803	glucan 1,4-alpha-m
29	274	10.1	428	2 T05521	alpha-amylase (EC

RESULT 1

A27705

alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase

C;Species: Bacillus sp.

C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

C;Accession: A27705

R;Tsukamoto, A.; Kimura, K.; Iehii, Y.; Takano, T.; Yamane, K.

Biochem. Biophys. Res. Commun. 151, 25-31, 1988

A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from an alkaloph

A;Reference number: A27705; MUID:88162814; PMID:3258152

A;Accession: A27705

A;Molecule type: DNA

A;Residues: 1-518 <TSU>

A;Cross-references: GB:M18862; NID:g142496; PID:AAA22231.1; PID:g142497

A;Experimental source: chromosomal DNA of strain 707

A;Note: amino end of mature protein also determined

C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amylolucifaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F;1-33/Domian: signal sequence #status predicted <SIG>

F;34-518/Product: alpha-amylase #status experimental <MAT>

F;236-369/Domian: alpha-amylase core homology <AMY>

F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted

F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 89.9%; Score 2440; DB 1; Length 518;

Best Local Similarity 87.6%; Pred. No. 4.1e-157; Indels 0; Gaps 0;

Matches 425; Conservative 32; Mismatches 28;

Qy 1 HHNGTNGTMMQYFEWYLPNDGNHWNRLDDAANLKSXGITAIVTTPPAWKGTSONDVGYGA 60

Db 34 HHNGTNGTMMQYFEWYLPNDGNHWNRLSDASNLKSXGITAIVTTPPAWKGSQNDVGYGA 93

Qy 61 YDLVDLGEFNQKGVTRTKYTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADGTETVNAV 120

Db 94 YDLVDLGEFNQKGVTRTKYTRNLQAAVTSLNKNGIQVYGDVVMNHKGGADATETVNAV 153

Qy 121 EVNFSNNOETSGEYATEAMTKDFPGKNNHSSFKRWVHFDGTDQDQSLQNKLYKF 180

Db 154 EVNPNNNQEVGTGYTTEAMTRFDGKNNHSSFKRWVHFDGTDQDQSLQNNRIYKF 213

Qy 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVTHELNMGVWYTTNTLNLDFRIDAVKH 240

Db 214 RGHGKAWDEVDTEGNYDYLMYADVDMDHPEVVMELRNMGVWYTTNTLNLDFRIDAVKH 273

Qy 241 IKYSFTRDWLTHTVNTTKGKPMFAVAEPFKNDLGAIEYNLNTKTSWNHVSFVDFPLHNLNA 300

Db 274 IKYSFTRDWINHVRVSATGKNMFAVAEPFKNDLGAIEYNLQKTNWNHVSFVDFPLHNLNA 333

QY 301 SNNGGYDMRNILNGSVVQKHPTHTAVTFVDNHDSDQGEALLESFVOQWFKPLAYALVLTRE 360
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 334 SKSGGNYDMRNINFGTVVQRHPSHAVTFVDNHDSDQGEALLESFVEWFKPLAYALVLTRE 393
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 361 QGYPSVFYGDYGYGPIPTHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNSG 420
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 394 QGYPSVFYGDYGYGPIPTHGVPAKMSKIDPILQARQKAYGKQNDYLDHNNIIGWTRGNTA 453
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQWRDITGNRTGTVTINADGWNFSVNGGSVS 480
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 454 HPNSGLATIMSDGAGGSKMVFGRNKAGQVSDITGNRTGTVTINADGWNFSVNGGSVS 513
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 481 VVYKQ 485
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 514 IWVWK 518
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
RESULT 2
A54541
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI1792)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C;Accession: A54541
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A;Reference number: A54541
A;Accession: A54541
A;Molecule type: DNA
A;Residues: 1-549 <JOR>
A;Cross-references: GB:X59476
A;Experimental source: Chromosomal DNA of strain DNI1792
C;Comment: Alpha-amylase Genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/DNA: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <Mat>
F;235-368/DNA: alpha-amylase core homology <AMV>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted
Query Match 70.4%; Score 1909.5; DB 1; Length 549;
Best Local Similarity 68.6%; Pred. No. 2.7e-121;
Matches 328; Conservative 69; Mismatches 80; Indels 1; Gaps 1;
QY 6 NGTMQYFEWYLDNDGNHNRDRDAAANLKSKITAWIIPPAKGTSONDVGGAYDLYD 65
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 39 NGTMQYFEWYLDNDGTLTWKVANEANLSSGITALWLPAYKGTSRSDVGGYDLYD 98
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 66 LGSEFNQGTVRTKYGTRNQLQAATVSLKXNGIOVYGDVNMVHKGAGDTGRIVNAVEVNR 125
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 99 LGSEFNQGTVRTKYGTGKAQYLQIAAHAAAGQVYADVDFDHKGAGDTGWDVDAVENPS 158
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 126 NRNQETSGEYAIBAWTKFDFPGRGNHSSFPKRWYHFDGTDQSRQLQNKYIKFRGTGK 185
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 159 DRNQEISGTYQIQAWTKFDFPGRGNTYSSPKRWYHFDGVDWDBSRKL-SRIYKFRGIGK 217
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 186 AWDWEVDVTENGNDYLMYADVMDHDEVIHELNRWGWYNTNLNLDGFRIDAVKHKYKSF 245
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 218 AWDWEVDVTENGNDYLMYADLDMHDEVTTELKNGKWYNTNIDGFRIDAVKHKYKSF 277
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 246 TRDLVTHRVNTGKPFVFAEAFKNDLGAJENYLNKTSWNHSPVDFVPLHVNLYNAGNSGG 305
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 278 FPDWLSVRSQTKPFLTVEGYNSYDINKLHNITKTDGTMSLFDAPLHNKFTASKSGG 337
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 306 YDMRNILNGSVVQKHPTHTAVTFVDNHDSDQGEALLESFVOQWFKPLAYALVLTREOGYPS 365
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
338 AFDMRTLMTNLTKMDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEGYPC 397
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 366 VFYGDYGYGPIPTHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNSHNSG 425
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 398 VFYGDYGYGPIPTHGVPAKMSKIDPLLIARRDYAGTQHDYLDHSDIIGWTRGEGTERKPGSG 457
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 426 LATIMSDGPGGNKMYVGNKAGQWRDITGNRTGTVTINADGWNFSVNGGSVSVMV 483
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 458 LAALITDGPGGSKMYVGNKAGKVFYDLTGNRSDIVTINSNGWGEFKVNGGSVSVWV 515
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
RESULT 3
ALBSL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus licheniformis
C;Date: 30-Jun-1987 #sequence_revision 24-Apr-1998 #text_change 15-Sep-2000
C;Accession: A91997; B24549; A91796; A21663; I39772; A26151; S53788; A00844
R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
J. Biochem. 98, 1147-1156, 1985
A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amyl
ases deduced from the DNA sequences.
A;Reference number: A91997; MUID:86111694; PMID:2418011
A;Accession: A91997
A;Molecule type: DNA
A;Residues: 1-162, 'R', 164-512 <YU>
A;Cross-references: GB:X03236; NID:G39551; PIDN:CAA26981.1; PID:G39552
A;Experimental source: ATCC 27811
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearotherm
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: B24549
A;Molecule type: DNA
A;Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
A;Cross-references: GB:M13256; NID:G142510; PIDN:AAA22240.1; PID:G142511
A;Experimental source: NCIB 8061
R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, 369-372, 1984
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A;Reference number: A91796; MUID:84185455; PMID:6609154
A;Accession: A91796
A;Molecule type: DNA
A;Residues: 1-104 <STE>
A;Cross-references: GB:K01984; NID:G142432; PIDN:AAA22193.1; PID:G142433
R;Sibakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amyl
A;Reference number: A21663; MUID:85076654; PMID:6334606
A;Accession: A21663
A;Molecule type: DNA
A;Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 8
A;Experimental source: Chromosomal DNA of ATCC 14580
A;Note: the authors translated the codon CGR for residue 48 as Gly and GAC for residue 64
R;Laoid, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A;Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
A;Reference number: I39773; MUID:89213924; PMID:2540150
A;Accession: I39774
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-29 <LAO>
A;Cross-references: GB:M26412; NID:G341477; PIDN:AAA22237.1; PID:G516590
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39772
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-32, 'I' <JOR>
A;Cross-references: GB:M62637; NID:G142498; PIDN:AAA22232.1; PID:G142499

Db 338 AFDMRTLMTNLTKMDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEGYPC 397
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 366 VFYGDYGYGPIPTHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTRGNSHNSG 425
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 398 VFYGDYGYGPIPTHGVPAKMSKIDPLLIARRDYAGTQHDYLDHSDIIGWTRGEGTERKPGSG 457
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 426 LATIMSDGPGGNKMYVGNKAGQWRDITGNRTGTVTINADGWNFSVNGGSVSVMV 483
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 458 LAALITDGPGGSKMYVGNKAGKVFYDLTGNRSDIVTINSNGWGEFKVNGGSVSVWV 515
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
RESULT 3
ALBSL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus licheniformis
C;Date: 30-Jun-1987 #sequence_revision 24-Apr-1998 #text_change 15-Sep-2000
C;Accession: A91997; B24549; A91796; A21663; I39772; A26151; S53788; A00844
R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
J. Biochem. 98, 1147-1156, 1985
A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amyl
ases deduced from the DNA sequences.
A;Reference number: A91997; MUID:86111694; PMID:2418011
A;Accession: A91997
A;Molecule type: DNA
A;Residues: 1-162, 'R', 164-512 <YU>
A;Cross-references: GB:X03236; NID:G39551; PIDN:CAA26981.1; PID:G39552
A;Experimental source: ATCC 27811
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearotherm
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: B24549
A;Molecule type: DNA
A;Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
A;Cross-references: GB:M13256; NID:G142510; PIDN:AAA22240.1; PID:G142511
A;Experimental source: NCIB 8061
R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, 369-372, 1984
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A;Reference number: A91796; MUID:84185455; PMID:6609154
A;Accession: A91796
A;Molecule type: DNA
A;Residues: 1-104 <STE>
A;Cross-references: GB:K01984; NID:G142432; PIDN:AAA22193.1; PID:G142433
R;Sibakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amyl
A;Reference number: A21663; MUID:85076654; PMID:6334606
A;Accession: A21663
A;Molecule type: DNA
A;Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 8
A;Experimental source: Chromosomal DNA of ATCC 14580
A;Note: the authors translated the codon CGR for residue 48 as Gly and GAC for residue 64
R;Laoid, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A;Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
A;Reference number: I39773; MUID:89213924; PMID:2540150
A;Accession: I39774
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-29 <LAO>
A;Cross-references: GB:M26412; NID:G341477; PIDN:AAA22237.1; PID:G516590
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39772
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-32, 'I' <JOR>
A;Cross-references: GB:M62637; NID:G142498; PIDN:AAA22232.1; PID:G142499

R;Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
J. Bacteriol. 149, 372-373, 1982
A;Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison of the amino acid sequence of the enzyme from Bacillus licheniformis and Bacillus subtilis
A;Reference number: A26151; MUID:82098050; PMID:6172418
A;Accession: A26151
A;Molecule type: protein
A;Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>
R;Machius, M.; Wiegand, G.; Huber, R.
J. Mol. Biol. 246, 545-559, 1995
A;Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.2 angstroms, residues 32-210,222-511
A;Reference number: S53788; MUID:95182462; PMID:7877175
A;Accession: S53788
A;Molecule type: protein
A;Residues: D', 220-227 <MAC>
A;Note: sequence represents amino end of an internal fragment created by a single enzymatic cleavage
R;Machius, M.; Wiegand, G.; Huber, R.
Submitted to the Brookhaven Protein Data Bank, July 1995
A;Reference number: A65206; PDB:1BPL
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210,222-511
R;Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.
Submitted to the Brookhaven Protein Data Bank, October 1996
A;Reference number: A66860; PDB:1VUS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210,222-511
C;Genetics:
A;Gene: amyl
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
A;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide hydrolase
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-512/Product: alpha-amylase #status experimental <AMY>
F;227-360/Domain: alpha-amylase core homology <AMY>
F;133,229,264/Binding site: calcium (Asn, Asp, His) #status experimental
F;260,290,357/Active site: Asp, Glu, Asp #status experimental
Query Match 70.2%; Score 1905; DB 1; Length 512;
Best Local Similarity 68.9%; Pred. No. 5e-121;
Matches 334; Conservative 65; Mismatches 76; Indels 10; Gaps 4;

Qy 6 NGTMMQFVFWLPNDGNHNRRLDDAANKLSKGTAVWIPPAWKGTSONDVGAYDLYD 65
Db 33 NGTMMQFVFWLPNDGNHNRRLDDAANKLSKGTAVWIPPAWKGTSONDVGAYDLYD 92
Qy 66 LGFENQKGTVRTKGTGRNQLQAQVTSLNKNGIQYGVGVVNMHKGAGDTEIVNAVEVNR 125
Db 93 LGFENQKGTVRTKGTGRNQLQAQVTSLNKNGIQYGVGVVNMHKGAGDTEIVNAVEVNR 152
Qy 126 NRNQTSGEYAEIAWTKDFPGRGNHNSFFKRWYHFDGTDWDSQRLQNKIYKFRGTGK 185
Db 153 DRNRVISGEHLIKAWTHFHPGRGSTYSDFKWHYHFDGTDWDSRKL-NRIYKFG--GK 209
Qy 186 AWDDEVDTENGNYDLYMYADVMDHPEVIELRWNGVWYVNTLNDGFRIDAVKHKYSF 245
Db 210 AWDDEVDTENGNYDLYMYADVMDHPEVIELRWNGVWYVNTLNDGFRIDAVKHKYSF 269
Qy 246 TRDWLTHVRNTTKPMFAVFAEFWKNLGAENYLNKTSWNHVSFVDFPLHYNLYNASNGG 305
Db 270 LRDMVNHVREKTKGEMFTVAEYQNDLGAENYLNKTSWNHVSFVDFPLHYNLYNASNGG 329
Qy 306 YYDMRNILNGSVVQKHPHTAVTFVDNHDSDQGEALSGVQWFKPLAYALVLTREQGYPS 365
Db 330 GYDMRKLNTSVSKPLKAVTFVDNHDSDQGEALSGVQWFKPLAYALVLTREQGYPS 389
Qy 366 VFYGDYGIPTHG-----VPAMKSKIDPLLAQRTFAYGTQHDYFDHHDIGWTRGNSG 420
Db 390 VFYGDYGIPTHG-----VPAMKSKIDPLLAQRTFAYGTQHDYFDHHDIGWTRGNSG 447
Qy 421 HPNSGLATIMSDGGGKNKMYVGNKAGQWRDITGNRTGTVTINADGWNFSVNGSGVS 480
Db 448 VANSGLAALITDGGPGKARMYVGRNQAGETWHDTIGNRSEPVVINSEGWGFFHYNGSGVS 507

Qy 481 VVVKQ 485
Db 508 IYVQR 512
RESULT 4
A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24549; I39501; I39770
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindie, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: A24549
A;Molecule type: DNA
A;Residues: 1-549 <GRA>
A;Cross-references: GB:M1325; NID:g142512; PIDN:AAA22241.1; PID:g142513
A;Experimental source: genomic DNA of strain NZ-3
R;Satoh, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A;Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distinct strains of Bacillus stearothermophilus
A;Reference number: I39501; MUID:88139156; PMID:3257753
A;Accession: I39501
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RES>
A;Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478
A;Experimental source: strain DY-5
A;Accession: I39770
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RE2>
A;Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A;Experimental source: strain 799
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the chromosome
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide hydrolase
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted
Query Match 70.0%; Score 1898.5; DB 1; Length 549;
Best Local Similarity 68.4%; Pred. No. 1.5e-120;
Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;

Qy 6 NGTMMQFVFWLPNDGNHNRRLDDAANKLSKGTAVWIPPAWKGTSONDVGAYDLYD 65
Db 39 NGTMMQFVFWLPNDGNHNRRLDDAANKLSKGTAVWIPPAWKGTSONDVGAYDLYD 98
Qy 66 LGFENQKGTVRTKGTGRNQLQAQVTSLNKNGIQYGVGVVNMHKGAGDTEIVNAVEVNR 125
Db 99 LGFENQKGTVRTKGTGRNQLQAQVTSLNKNGIQYGVGVVNMHKGAGDTEIVNAVEVNR 158
Qy 126 NRNQTSGEYAEIAWTKDFPGRGNHNSFFKRWYHFDGTDWDSQRLQNKIYKFRGTGK 185
Db 159 DRNQEISGTQIQIQAQVTSLNKNGIQYGVGVVNMHKGAGDTEIVNAVEVNR 217
Qy 186 AWDDEVDTENGNYDLYMYADVMDHPEVIELRWNGVWYVNTLNDGFRIDAVKHKYSF 245
Db 218 AWDDEVDTENGNYDLYMYADVMDHPEVIELRWNGVWYVNTLNDGFRIDAVKHKYSF 277
Qy 246 TRDWLTHVRNTTKPMFAVFAEFWKNLGAENYLNKTSWNHVSFVDFPLHYNLYNASNGG 305

Db 278 FPDWLSYVRSGTQKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFTASKSGG 337
QY 306 YDMRNLINGSVQKPTHTAVTFVDNHDSPGRLSFFVQWFKPLAYALVLTREQGYPS 365
Db 338 AFMSILMNWTLMKDQPTLAVTFVDNHDTEPGALQSWDPWPKPLAYAFILTRQSGYPC 397
QY 366 VFYGDYGIPTGTHGVPAWMSKIDPDLQAROTFAYGTQHDYFDHDDIIGWTREGNSSHPNSG 425
Db 398 VFYGDYGIPTGTHGVPAWMSKIDPDLQAROTFAYGTQHDYFDHDDIIGWTREGVTEKPGSG 457
QY 426 LATIMSDGPGGNKMWYGVKNAQGVWRDITGNRTGTVTINADGWGNSVNGGVSVMV 483
Db 458 LAALITDGGGSKMWYGVKQHAGKVFYDLTGNSRSDVTITNSDGGFKVNGGVSVMV 515
RESULT 5
A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N;Alternate names: 1,4-alpha-D-glucan glucohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; I39777
R;Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Accession: A24436
A;Molecule type: DNA
A;Residues: 1-549 <NA>
A;Cross-references: GB:M11450
A;Experimental source: plasmid pAT5
A;Note: amino end of the mature protein also determined
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2465757
A;Accession: I39777
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-45 <RES>
A;Cross-references: GB:M62638; NID:gl42514; PIDN:AAA22242.1; PID:gl42515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Gene: amyS
A;Genome: plasmid
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted
Query Match 69.7%; Score 1892.5; DB 1; Length 549;
Best Local Similarity 68.2%; Pred. No. 3.8e-120;
Matches 326; Conservative 70; Mismatches 81; Indels 1; Gaps 1;
QY 6 NGTMMQYFEWYLPNDGNHNNRLRDLAANKSGKITAWIPPAWKGTSQNDVGAYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLTWTKVANEANLSSLGITALLWLPAYKGTSRSDVGVTYDLYD 98
QY 66 LGSEFNKGTVRTYKTRNLQAAVTSLNKNGIQYGDVGVWNNHKGADGTIVNAVEVNR 125
Db 99 LGSEFNKGAVRTYKGTGAQYLOIAQAAHAGMQVYADVDFHKGADGTVEVDVAVNPS 158
QY 126 NRNQETSGEVAIEAWTKFDPGPGNNHSSPKFWYHFDGTDWQSRQLQNKIKYKFGTGK 185
Db 159 DRNQELSGTVQIQAWTKFDPGPGNNYSSPKFWYHFDGVDWDESKL-SRIYKFRGIGK 217
QY 186 AWDWEVDVTENGNYDLYMADVDMDHPEVIHELNRWGWYVNTNLNLDGFRIDAVKHKYSF 245

Db 218 AWDWEVDVTENGNYDLYMADVDMDHPEVVTLSKWKYVNTNIDGFRIDAVKHKYSF 277
QY 246 TRDMLTHVNTTCKPMFAVAFKNDLGALENLNTKSNHNSVDFVPLHYNLNASNSGG 305
Db 278 FPDWLSYVRSGTQKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFTASKSGG 337
QY 306 YDMRNLINGSVQKPTHTAVTFVDNHDSPGRLSFFVQWFKPLAYALVLTREQGYPS 365
Db 338 AFMSILMNWTLMKDQPTLAVTFVDNHDTEPGALQSWDPWPKPLAYAFILTRQSGYPC 397
QY 366 VFYGDYGIPTGTHGVPAWMSKIDPDLQAROTFAYGTQHDYFDHDDIIGWTREGNSSHPNSG 425
Db 398 VFYGDYGIPTGTHGVPAWMSKIDPDLQAROTFAYGTQHDYFDHDDIIGWTREGVTEKPGSG 457
QY 426 LATIMSDGPGGNKMWYGVKNAQGVWRDITGNRTGTVTINADGWGNSVNGGVSVMV 483
Db 458 LAALITDGGGSKMWYGVKQHAGKVFYDLTGNSRSDVTITNSDGGFKVNGGVSVMV 515
RESULT 6
ALASN
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens
N;Alternate names: 1,4-alpha-D-glucan glucohydrolase
C;Species: Bacillus amylioliquefaciens
C;Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A92389; I39756; I39763; A00843
R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
J. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced fr
A;Reference number: A92389; MUID:83108808; PMID:6185474
A;Contents: PUB110
A;Accession: A92389
A;Molecule type: DNA
A;Residues: 1-514 <TAK>
A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:gl42428; PIDN:AAA2219
R;Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.
A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307
A;Molecule type: protein
A;Residues: 32-53, 'I', '55-63, 'I', '65-78, 'D', '80-83, 'S', '85-222 <CHU>
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A;Reference number: I39756; MUID:82051296; PMID:6170539
A;Accession: I39756
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Cross-references: EMBL:V00092; NID:gl39297; PIDN:CAA23430.1; PID:gl39298
R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karanen, S.
Gene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its ow
A;Reference number: I39763; MUID:88137952; PMID:2830166
A;Accession: I39763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-39 <RES>
A;Cross-references: GB:M18424; NID:gl42430; PIDN:AAA22192.1; PID:gl42431
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-362/Domain: alpha-amylase core homology <AMY>
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
Query Match 68.2%; Score 1850; DB 1; Length 514;

Db 302 GANYDLRGIFDTSVLVELKPKDCAVTFVDNHDTRQQALESSTVEWFKPAAYALILLRQDGL 361
Qy 364 PSVFGYDYGIP-THGVPAMKSKIDPLLOARQTFAYGTQHDYFDHDIIGWTRGNSHP 422
Db 362 PCVFGYDYGISGQAQDFEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRSG--AEN 419
Qy 423 NSGLATMSDPCGNKMYGKNAQGWDRITGNRTGTVTINADGWNFSVNGSGSVW 482
Db 420 QSPFVILISNDQENSKMFVGQEWNTQTFVDLLGSHQGVTDIBEGYGFVPSARSVW 479
RESULT 11
AH2079
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH2079
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-492 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073889.1; PID:g17131281; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2190
C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
Query Match 45.78; Score 1239; DB 2; Length 492;
Best Local Similarity 48.48; Pred. No. 4e-76;
Matches 238; Conservative 79; Mismatches 157; Indels 18; Gaps 6;
Qy 6 NGTMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTSQ-N-DVGYGAYDLY 64
Db 5 NGTMQYFEWYLPNDGNLMSKVEASAPELADAGFTAMWLPAYKGFAGSDVGVGYDLP 64
Qy 65 DLGEFNQKQVTRTKYGRNQLQAQAVTSLKNGIQVYGVVNMHKGADGTEIVNAVVRN 124
Db 65 DLGEFDQKGSVTRTKYGRQVLDVAVKSLQTHGLQVYADAVLNHKGMDGDAVETPKATFPQ 124
Qy 125 SNRQETSCEYAIEAWTKFDFPGRGNHSSFKRWVHFDGTDWDQ-SRQONKIYKFRGT 183
Db 125 DRLNPKGGLQDKITYTHYFPGRQGYKSNFEMHWHFDAVDYNEYSGRDSTRVYLLE-- 182
Qy 184 GKAWDWEVDTEGNYDLYMAYADVMDHPEVIHELNRWGVWYTNLNDGFRIDAVKHKY 243
Db 183 GKAFDDVVALEKGNFAYLMGCDLDFQNEWRGEVYTWGKWLDTTKYDGGFRIDAKHIST 242
Qy 244 SFTRDMLTHVRNTTGMFMAFAEFKNDLGAENLYLNKTSWNHVSFVDFVPLHLYNLSNS 303
Db 243 WFPPEWIDALERHAGKDLFWGGEVYNDINTLLWYDVAVRGKVSFVDFVPLHLYNFHQASKS 302
Qy 304 GGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTREQGY 363
Db 303 GGNVDERRILDGTMQQRPHATVTFVFNHDSQPLQALESVVEFWFKPLAYALVLTREQGY 362
Qy 364 PSVFGYDYGIPTHG-----VPAMKSKIDPLLOARQTFAYGTQHDYFDHDIIG 412
Db 363 PCVFDHAYDGAEDWKGNGRNYNIFMPSHRWIIDKLLYARKHAYGFPQNYLDHWNITIG 422
Qy 413 WTRGNSHSPNSGLATMSDPCGNKMYGKNAQGWDRITGNRTGTVTINADGWNFS 472
Db 423 WTRLGADHP-QGNVATMSDSEIGKMEVGKPKTKFI--DLTEHIKEAVYTNWGWGEF 479
Qy 473 SVNGSGSVWVWK 484
Db 480 RCLGSGSVWVWQ 491

RESULT 12

C86781

alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: C86781

R:Bohlooti, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: C86781

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-491 <STO>

A:Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: amyl

C:Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 41.58; Score 1127; DB 2; Length 491;

Best Local Similarity 42.34; Pred. No. 1.4e-68;

Matches 202; Conservative 99; Mismatches 172; Indels 4; Gaps 3;

Qy 8 TMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVWIPPAWKGTS-QNDVGYGAYDLYDL 66

Db 3 TILQAFWYLPSPDSQHNWNIKENIPDLKLGFSGLWLPAPASKASGVEDVGYTYDLDL 62

Qy 67 GFNQKQVTRTKYGRNQLQAQAVTSLKNGIQVYGVVNMHKGADGTEIVNAVVRN 126

Db 63 GFQDKGTIPTKGTDEYLDLINTLHNNIEVYADVFNHMGADETETIADIKABDN 122

Qy 127 RNQETSCEYAIEAWTKFDFPGRGNHSSFKRWVHFDGTDWDQSRQONKIYKFRGTGA 186

Db 123 HLHNIENKKTVEWTKFTFFPGRQGYDNYITWHRFTGIDYDE-RKNQEILEPE--GHE 179

Qy 187 WDEVDTEGNYDLYMAYADVMDHPEVIHELNRWGVWYTNLNDGFRIDAVKHKYSFT 246

Db 180 WDEVDSENNFDYLMGADLDFSVSEVQEKWGFSEWTKIDGFRIDAKHIDKYP 239

Qy 247 RDMLTHTVRNTTGMFMAFAEFKNDLGAENLYLNKTSWNHVSFVDFVPLHLYNLSNSGGY 306

Db 240 DKWLEQRAKQLDRKLFVGEVWSDDLGKLEYLEQSSDRQLQDFVPLHFNKKEASTNGE 299

Qy 307 YDMRNILNGSVQKHPHATVTFVDNHDSPQGEALESFVQQWFKPLAYALVLTREQGYPSV 366

Db 300 FDMRTLLFDHTLTASQPELSVTFVDNHDTRQQALESWIPAWFKPEHAYSLILRKKETPTV 359

Qy 367 FYGDIYGYIPTHGVPAMKSKIDPLLOARQTFAYGTQHDYFDHDIIGWTRGNSHSPNSGL 426

Db 360 FWGDLYGIPSHNVFVGNLRTMLARKDSEFURENDYFDHDIIGWTRGNSHSPNSGL 419

Qy 427 ATMSDPCGNKMYGKNAQGWDRITGNRTGTVTINADGWNFSVNGSGSVWV 483

Db 420 SCILTNKSGSKMIDKAYAGKYIDLFGRHEIPITLDQNGAEFYVNDGSGSVWV 476

RESULT 13

G98247

cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacteri

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002

C:Accession: G98247

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: G98247

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-506 <KUR>

A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:gl15159379; GSPDB:GN00170
C;Genes: AGR L1863
A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 40.4%; Score 1097; DB 2; Length 506;
Best Local Similarity 45.1%; Pred. No. 1.6e-66;
Matches 223; Conservative 76; Mismatches 178; Indels 18; Gaps 7;

QY 3 NGTNGTMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSON-DVGYGAY 61
DB 11 NMAGRITLQFFHWYYPDGGKLSWAEKASLAKMGITDVMLEPAYKAAGGSVGYDY 70
QY 62 DLYDLGEFNOKGTVRTKYGRNOLQAAVTSLKNGIQVYGDVVMNHKGGADGTEIVNAVE 121
DB 71 DLFDLGEGFDQGVATKYGDRAALEHAGKTLKONGIRVHIDVVLNHNKGADEKEKVRVR 130
QY 122 VNRSNRQETSGBEYAJEAWTKFDPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF- 180
DB 131 VNPDDRDTIDDEPPALAYTRFTFPGRNGKHSKFIWDLKCFSGVDHIE-EPTEDGIFRLV 189
QY 181 --RGTKANDWEVDTENGNDYLMYADVMDHPEVHELNRNMGVWYNTNLNLDGFRIDAV 238
DB 190 NEYGDGE-WNEEVDQENGFYDLMGADVEFRNRAVYELKYWGRWLSBQVQVDFRLDAA 248
QY 239 KHLKYSFTRDLWLTNRNTTKPMFAVAEFWKNDLGAJENYLNKTSWNHVSFVDPVPLHNYL 298
DB 249 KHLPAWFFRDVWGHMRETVDPLFVVAEYVHPDLEALKSYLELDVKQLMLFDVALHHSFH 308
QY 299 NASNSGGYDMRNILNGSVQKHPTHAFTVDNHDSPQGEALSFVQOWFKPLAYALVLT 358
DB 309 DASKQGGDFMRSIFDGLSVSAVPDHAFTLVNDHDTQPLQSLAPVPEWPKPLAYAILL 368
QY 359 REOGYPSVFGDYVG--IPTHGVPAKSKID-----PLLOAROTPAYQTHDHYDHH 408
DB 369 REEGVPCVFPDLEFGTSYDTGTGNDGNEYKIDIPAIECLPKLIARSFANGPQTDIFDDA 428
QY 409 DIIGWTREGNSHPNSGLATIMSDGPGKNWYVGNKAGQVWRDITGNRTGTVTINADG 468
DB 429 SCTAFIRHGTADAP--GCVVMSNGEPGEQADLGPERRAGSVWRDFLGHRHEHITLDESG 486
QY 469 WGNFNSVNGGSVSVWV 483
DB 487 KGTFFPINGGSVSVWV 501

RESULT 14
AD3038
alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3038
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gilet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-495 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAI44722.1; PID:gl17742354; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: amyA
A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 40.4%; Score 1096; DB 2; Length 495;

Best Local Similarity 45.3%; Pred. No. 1.8e-66;
Matches 222; Conservative 76; Mismatches 174; Indels 18; Gaps 7;

QY 8 TMQYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSON-DVGYGAYDYL 66
DB 5 TILQFFHWYYPDGGKLSWAEKASLAKMGITDVMLEPAYKAAGGSVGYDYDLDL 64
QY 67 GBFNOKGTVRTKYGRNOLQAAVTSLKNGIQVYGDVVMNHKGGADGTEIVNAVEVNRN 126
DB 65 GSFQDKGTATKYGDRAALEHAGKTLKONGIRVHIDVVLNHNKGADEKEKVRVR 124
QY 127 RQETSGBEYAJEAWTKFDPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF---RGT 183
DB 125 RTDIDDEPPALAYTRFTFPGRNGKHSKFIWDLKCFSGVDHIE-EPTEDGIFRLVNEYGD 183
QY 184 GKAWDEWVDTENGNDYLMYADVMDHPEVHELNRNMGVWYNTNLNLDGFRIDAVKHKY 243
DB 184 GE-WNEEVDQENGFYDLMGADVEFRNRAVYELKYWGRWLSBQVQVDFRLDAAHIPA 242
QY 244 SETRWLTHVRNTTKPMFAVAEFWKNDLGAJENYLNKTSWNHVSFVDPVPLHNYLNASNS 303
DB 243 WFFRDVWGHMRETVDPLFVVAEYVHPDLEALKSYLELDVKQLMLFDVALHHSFHDASKQ 302
QY 304 GGYDMRNILNGSVQKHPTHAFTVDNHDSPQGEALSFVQOWFKPLAYALVLTREOGY 363
DB 303 GGDFFMRSIFDGLSVSAVPDHAFTLVNDHDTQPLQSLAPVPEWPKPLAYAILLREEGV 362
QY 364 PSVFYGDYVG--IPTHGVPAKSKID-----PLLOAROTPAYQTHDHYDHHDIIGW 413
DB 363 PCVFPDLEFGTSYDTGTGNDGNEYKIDIPAIECLPKLIARSFANGPQTDIFDDASCI 422
QY 414 TREGNSHPNSGLATIMSDGPGKNWYVGNKAGQVWRDITGNRTGTVTINADGWNFS 473
DB 423 IRHGTADAP--GCVVMSNGEPGEQADLGPERRAGSVWRDFLCHREHITLDESGKGTFF 480
QY 474 VNGGSVSVWV 483
DB 481 TNGGSVSVWV 490

RESULT 15
B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Salmonella typhimurium
C;Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: B45738
R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A;Reference number: A45738; MUID:93015717; PMID:1400215
A;Accession: B45738
A;Molecule type: DNA
A;Residues: 1-494 <RAH>
A;Cross-references: GB:L01643; NID:gl54043; PIDN:AAA27110.1; PID:gl54045
C;Genetics:
A;Gene: amyA
A;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F;202-335/Domain: alpha-amylase core homology <AMY>
F;239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.6%; Score 1076; DB 1; Length 494;
Best Local Similarity 42.7%; Pred. No. 4e-65;
Matches 210; Conservative 81; Mismatches 183; Indels 18; Gaps 6;

QY 6 NGTMOYFEWYLPNDGNHNRRLRDDAANKLSKGITAVWIPPAWKGTSON-DVGYGAYDYL 64
DB 3 NPTLLQYFHWYYPDGGKLSWAEKASLAKMGITDVMLEPAYKAAGGSVGYDYDLDL 62

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-2
Perfect score: 2714
Sequence: 1 HHNGTNGTMMQYFEWYLPND.....ADGMNFSVNGSVSVWVKQ 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/CTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2714	100.0	485	9	US-09-769-864-1
2	2714	100.0	485	9	US-09-769-864-7
3	2714	100.0	485	9	US-09-854-346-2
4	2714	100.0	485	9	US-09-902-188A-1
5	2714	100.0	485	9	US-09-918-543-2
6	2714	100.0	485	9	US-09-795-211-1
7	2714	100.0	485	10	US-09-925-576C-2
8	2714	100.0	485	12	US-10-665-667-1
9	2714	100.0	485	12	US-10-665-667-7
10	2714	100.0	485	12	US-10-665-648-1
11	2714	100.0	485	12	US-10-327-837-1
12	2714	100.0	485	12	US-10-327-837-7
13	2714	100.0	485	14	US-10-184-771-12
14	2714	100.0	485	16	US-10-477-725-2
15	2613	96.3	516	9	US-09-986-676A-2

16	2613	96.3	516	9	US-09-971-611-2	Sequence 2, Appli
17	2613	96.3	516	16	US-10-399-161-8	Sequence 8, Appli
18	2456	90.5	516	16	US-10-343-212-2	Sequence 2, Appli
19	2448	90.2	485	9	US-09-769-864-2	Sequence 2, Appli
20	2448	90.2	485	9	US-09-769-864-8	Sequence 8, Appli
21	2448	90.2	485	9	US-09-854-346-4	Sequence 4, Appli
22	2448	90.2	485	9	US-09-902-188A-2	Sequence 2, Appli
23	2448	90.2	485	9	US-09-918-543-4	Sequence 4, Appli
24	2448	90.2	485	9	US-09-795-211-2	Sequence 2, Appli
25	2448	90.2	485	10	US-09-925-576C-4	Sequence 4, Appli
26	2448	90.2	485	12	US-10-665-667-2	Sequence 2, Appli
27	2448	90.2	485	12	US-10-665-667-8	Sequence 8, Appli
28	2448	90.2	485	12	US-10-025-648-2	Sequence 2, Appli
29	2448	90.2	485	12	US-10-327-837-2	Sequence 2, Appli
30	2448	90.2	485	12	US-10-327-837-8	Sequence 8, Appli
31	2448	90.2	485	16	US-10-477-725-4	Sequence 4, Appli
32	2440	89.9	485	9	US-09-769-864-6	Sequence 6, Appli
33	2440	89.9	485	9	US-09-854-346-13	Sequence 13, Appli
34	2440	89.9	485	9	US-09-902-188A-7	Sequence 7, Appli
35	2440	89.9	485	10	US-09-925-576C-13	Sequence 13, Appli
36	2440	89.9	485	12	US-10-665-667-6	Sequence 6, Appli
37	2440	89.9	485	12	US-10-025-648-7	Sequence 7, Appli
38	2440	89.9	485	12	US-10-327-837-6	Sequence 6, Appli
39	2440	89.9	485	16	US-10-477-725-13	Sequence 13, Appli
40	2429	89.5	485	9	US-09-854-346-12	Sequence 12, Appli
41	2429	89.5	485	9	US-09-918-543-12	Sequence 12, Appli
42	2429	89.5	485	10	US-09-925-576C-12	Sequence 12, Appli
43	2429	89.5	485	12	US-10-327-837-24	Sequence 24, Appli
44	2429	89.5	485	12	US-10-327-837-26	Sequence 26, Appli
45	2429	89.5	485	14	US-10-209-812-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-769-864-1
; Sequence 1, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-769-864-1

Query Match 100.0%; Score 2714; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVMIPPAAWKTSQNDVGGA 60

Db 1 HHNGTNGTMMQYFEWYLPNDGNHNRRLRDAANLKSIGITAVMIPPAAWKTSQNDVGGA 60

Qy 61 YDLIDLEFNOKQTVRTKYTRNLQAAVTSLNKNGIQVYGVVMMHKGADGTEIVNAV 120

Db 61 YDLIDLEFNOKQTVRTKYTRNLQAAVTSLNKNGIQVYGVVMMHKGADGTEIVNAV 120

Qy 121 EVNRSNRNQTSGEYATIAWTKDFPGRGNNHSSFKWRVYHFDGTDQSRQLQNKIYKF 180

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Db 121 EVNRSNRNQTSGEYAEAWTKDFPGRGNHSSFKWRVYHFDGTDWDSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWYVYTNLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWYVYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
Db 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSYS 480
Db 421 HPNSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSYS 480
Qy 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 2
US-09-769-864-7
; Sequence 7, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-7

Query Match 100.0%; Score 2714; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVMIPPAAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVMIPPAAWKGTSONDVGYGA 60
Qy 61 YDLYLGEFNGKQVTRTKYGRNQLQAATVSLKNGIGQYVGDVVMNHKGADGTEIVNAV 120
Db 61 YDLYLGEFNGKQVTRTKYGRNQLQAATVSLKNGIGQYVGDVVMNHKGADGTEIVNAV 120
Qy 121 EVNRSNRNQTSGEYAEAWTKDFPGRGNHSSFKWRVYHFDGTDWDSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEAWTKDFPGRGNHSSFKWRVYHFDGTDWDSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWYVYTNLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWYVYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
Db 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
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Qy 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
Db 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSYS 480
Db 421 HPNSGLATIMSDGPGGNKMWYGVKNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSYS 480
Qy 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 3
US-09-854-346-2
; Sequence 2, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-854-346-2

Query Match 100.0%; Score 2714; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVMIPPAAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLDDAANLKSIGITAVMIPPAAWKGTSONDVGYGA 60
Qy 61 YDLYLGEFNGKQVTRTKYGRNQLQAATVSLKNGIGQYVGDVVMNHKGADGTEIVNAV 120
Db 61 YDLYLGEFNGKQVTRTKYGRNQLQAATVSLKNGIGQYVGDVVMNHKGADGTEIVNAV 120
Qy 121 EVNRSNRNQTSGEYAEAWTKDFPGRGNHSSFKWRVYHFDGTDWDSRQLQNKIYKF 180
Db 121 EVNRSNRNQTSGEYAEAWTKDFPGRGNHSSFKWRVYHFDGTDWDSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWYVYTNLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLYADVDMDHPEVHELRLNKGWYVYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Db 241 IKYSFTRDMLTHVRNTTGKPMFAVAFWKNDLGAENYLNKTSWNHNSVFDVPLHYNLNA 300
Qy 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVQKHPTAVTFVDNHDSPQCEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
Db 361 QGYPSPFYGDYIGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNS 420
```

Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNSVNGSGVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNSVNGSGVS 480
Qy 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 4
US-09-902-188A-1
; Sequence 1, Application US/09902188A
; Patent No. US20020098996A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; Svendsen, Allan
; Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: No. US20020098996A1o No. US20020098996A1disk of No. US20020098996A1
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk.
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/902,188A
; FILING DATE: 10-Jul-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/354,191
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-902-188A-1

Query Match 100.0%; Score 2714; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGNHWNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMQYFEWYLPNDGNHWNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLYDLGEFQKGTVRTKGYTRNLQAAVTSKNGIGIQQVYGDVVMNHKGGADGTEIVNAV 120
Db 61 YDLYDLGEFQKGTVRTKGYTRNLQAAVTSKNGIGIQQVYGDVVMNHKGGADGTEIVNAV 120
Qy 121 EVNRSNRNQETSGEYATEAWTKFDPGCGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYATEAWTKFDPGCGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNGYDLYMYADVMDHPEVITHELNRNMGVWYNTNTNLNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDLYMYADVMDHPEVITHELNRNMGVWYNTNTNLNLDGFRIDAVKH 240
Qy 241 IKYSFTDRDLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLNA 300
Db 241 IKYSFTDRDLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLNA 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTHTAVTFVNDHDSQPGEALSFVQOQFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTHTAVTFVNDHDSQPGEALSFVQOQFKPLAYALVLTRE 360

Db 181 RGTGKAWDEVDTEGNGYDLYMYADVMDHPEVITHELNRNMGVWYNTNTNLNLDGFRIDAVKH 240
Qy 241 IKYSFTDRDLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLNA 300
Db 241 IKYSFTDRDLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLNA 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTHTAVTFVNDHDSQPGEALSFVQOQFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTHTAVTFVNDHDSQPGEALSFVQOQFKPLAYALVLTRE 360
Qy 361 QGYPSVFYGYGIPTHGVPAKMSKIDPLQAROTFAYGTOHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFYGYGIPTHGVPAKMSKIDPLQAROTFAYGTOHDYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNSVNGSGVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWGNSVNGSGVS 480
Qy 481 VVVKQ 485
Db 481 VVVKQ 485

RESULT 5
US-09-918-543-2
; Sequence 2, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-918-543-2

Query Match 100.0%; Score 2714; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGNHWNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMQYFEWYLPNDGNHWNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLYDLGEFQKGTVRTKGYTRNLQAAVTSKNGIGIQQVYGDVVMNHKGGADGTEIVNAV 120
Db 61 YDLYDLGEFQKGTVRTKGYTRNLQAAVTSKNGIGIQQVYGDVVMNHKGGADGTEIVNAV 120
Qy 121 EVNRSNRNQETSGEYATEAWTKFDPGCGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYATEAWTKFDPGCGNNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNGYDLYMYADVMDHPEVITHELNRNMGVWYNTNTNLNLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNGYDLYMYADVMDHPEVITHELNRNMGVWYNTNTNLNLDGFRIDAVKH 240
Qy 241 IKYSFTDRDLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLNA 300
Db 241 IKYSFTDRDLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLNA 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTHTAVTFVNDHDSQPGEALSFVQOQFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTHTAVTFVNDHDSQPGEALSFVQOQFKPLAYALVLTRE 360

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QY 361 QGYPSPFYGDYGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS 420
|||||
DB 361 QGYPSPFYGDYGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480
|||||
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480

QY 481 VWVKQ 485
|||||
DB 481 VWVKQ 485

RESULT 6
US-09-795-211-1
; Sequence 1, Application US/09795211
; Publication No. US20020183226A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Kasturi, Chandrika
; APPLICANT: Wandstrat, Mark E.
; APPLICANT: Song, Brian X.
; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZY
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: Detergent Composition
; CURRENT APPLICATION NUMBER: US/09/795,211
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: alkaliphilic bacillus
US-09-795-211-1

Query Match 100.0%; Score 2714; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
|||||
DB 1 HNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60

QY 61 YDLYDLGEFNOKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMNHKGGADGTEIVNAV 120
|||||
DB 61 YDLYDLGEFNOKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMNHKGGADGTEIVNAV 120

QY 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180
|||||
DB 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTEGNYDYLMDVDMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240
|||||
DB 181 RGTGKAWDEVDTEGNYDYLMDVDMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDWLTHVRNTTGKPMFAVABFWKNDLGAENLYLNKTSWNHVSFVDPVPLHNLNA 300
|||||
DB 241 IKYSFTRDWLTHVRNTTGKPMFAVABFWKNDLGAENLYLNKTSWNHVSFVDPVPLHNLNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPHATVTFVDNHDSDQGEALESFVQQWFKPLAYALVLTRE 360
|||||
DB 301 SNSGGYDMRNILNGSVVQKHPHATVTFVDNHDSDQGEALESFVQQWFKPLAYALVLTRE 360

QY 361 QGYPSPFYGDYGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS 420
|||||
DB 361 QGYPSPFYGDYGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480
|||||
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480

QY 481 VWVKQ 485
|||||
DB 481 VWVKQ 485
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DB 481 VWVKQ 485
|||||

RESULT 7
US-09-925-576C-2
; Sequence 2, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-925-576C-2

Query Match 100.0%; Score 2714; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
|||||
DB 1 HNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60

QY 61 YDLYDLGEFNOKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMNHKGGADGTEIVNAV 120
|||||
DB 61 YDLYDLGEFNOKGTVRTKYGTRNQLQAQVTSLNKNGIQVYGVDMNHKGGADGTEIVNAV 120

QY 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180
|||||
DB 121 EVNRSNRNQETSGEYAEAWTKFDFPGRGNHSSFKRWYHFDGTDWDQSRQLQNKIYKF 180

QY 181 RGTGKAWDEVDTEGNYDYLMDVDMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240
|||||
DB 181 RGTGKAWDEVDTEGNYDYLMDVDMDHPEVHELNRNGVWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDWLTHVRNTTGKPMFAVABFWKNDLGAENLYLNKTSWNHVSFVDPVPLHNLNA 300
|||||
DB 241 IKYSFTRDWLTHVRNTTGKPMFAVABFWKNDLGAENLYLNKTSWNHVSFVDPVPLHNLNA 300

QY 301 SNSGGYDMRNILNGSVVQKHPHATVTFVDNHDSDQGEALESFVQQWFKPLAYALVLTRE 360
|||||
DB 301 SNSGGYDMRNILNGSVVQKHPHATVTFVDNHDSDQGEALESFVQQWFKPLAYALVLTRE 360

QY 361 QGYPSPFYGDYGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS 420
|||||
DB 361 QGYPSPFYGDYGIPTHGVPAMSKIDPLQARQTFAYGTQHDYFDHHDIIIGWTREGNSS 420

QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480
|||||
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNSVNGSGVS 480

QY 481 VWVKQ 485
|||||
DB 481 VWVKQ 485

RESULT 8
US-10-665-667-1
; Sequence 1, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
```

```
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRN
; ORGANISM: Bacillus
US-10-665-667-1

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLYLDFEFNKGKTVRTKYGTRNQLQAAVTSKNGIQVYGVVNNHKGAGDGTETINAV 120
Db 61 YDLYLDFEFNKGKTVRTKYGTRNQLQAAVTSKNGIQVYGVVNNHKGAGDGTETINAV 120
Qy 121 EVNRSNRNQETSGEYATEAMTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYATEAMTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVNTTCKPMFAVAEFWKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Db 241 IKYSFTRDWLTHVNTTCKPMFAVAEFWKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Db 361 QGYSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 9
US-10-665-667-7
; Sequence 7, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
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; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRN
; ORGANISM: Bacillus sp.
US-10-665-667-7

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
Qy 61 YDLYLDFEFNKGKTVRTKYGTRNQLQAAVTSKNGIQVYGVVNNHKGAGDGTETINAV 120
Db 61 YDLYLDFEFNKGKTVRTKYGTRNQLQAAVTSKNGIQVYGVVNNHKGAGDGTETINAV 120
Qy 121 EVNRSNRNQETSGEYATEAMTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYATEAMTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Qy 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLNDGFRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLMYADVDMDHPEVHELNRNMGVWYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVNTTCKPMFAVAEFWKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Db 241 IKYSFTRDWLTHVNTTCKPMFAVAEFWKNDLGAENLANKTSWNHVSFVQWFKPLAYALVLTRE 300
Qy 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNILNGSVVQKHPTAVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
Qy 361 QGYSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Db 361 QGYSVFYGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTHQDHYFDHDDIIGWTREGNSS 420
Qy 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTGTINADGWNFSVNGGSVS 480
Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 10
US-10-025-648-1
; Sequence 1, Application US/10025648
; Publication No. US20030064908A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; Svendsen, Allan
; Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/025,648
/ FILING DATE: 19-Dec-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/600,656
/ FILING DATE: 13-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lambiris, Elias J.
/ REGISTRATION NUMBER: 33,728
/ REFERENCE/DOCKET NUMBER: 4318.204-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 867 0123
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 485 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-025-648-1

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
DB 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAI EAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYAI EAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDWEVDTENGNYDYLMDYADVMDHPHPEVIHELNRWGVWYTNLTNLDGFRIDAVKH 240
DB 181 RGTGKAWDWEVDTENGNYDYLMDYADVMDHPHPEVIHELNRWGVWYTNLTNLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHSHVFDVPLHYNLNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHSHVFDVPLHYNLNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
DB 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 11
US-10-327-837-1
; Sequence 1, Application US/10327837
; Publication No. US20030211958A1

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/025,648
/ FILING DATE: 19-Dec-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/600,656
/ FILING DATE: 13-FEB-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lambiris, Elias J.
/ REGISTRATION NUMBER: 33,728
/ REFERENCE/DOCKET NUMBER: 4318.204-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 867 0123
/ TELEFAX: 212 867 0298
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 485 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-025-648-1

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
DB 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAI EAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYAI EAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDWEVDTENGNYDYLMDYADVMDHPHPEVIHELNRWGVWYTNLTNLDGFRIDAVKH 240
DB 181 RGTGKAWDWEVDTENGNYDYLMDYADVMDHPHPEVIHELNRWGVWYTNLTNLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHSHVFDVPLHYNLNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHSHVFDVPLHYNLNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
DB 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 12
US-10-327-837-7
; Sequence 7, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-1

GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-1

Query Match      100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
DB 61 YDLYDLGEFNGKQGTVRTKYGTRNQLQAAVTSLNKNGIQVYGDVVMNHKGGADGTEIVNAV 120
QY 121 EVNRSNRNQTSGEYAI EAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
DB 121 EVNRSNRNQTSGEYAI EAWTKFDFPGRGNHNSFKRWYHFDGTDWDQSRQLQNKIYKF 180
QY 181 RGTGKAWDWEVDTENGNYDYLMDYADVMDHPHPEVIHELNRWGVWYTNLTNLDGFRIDAVKH 240
DB 181 RGTGKAWDWEVDTENGNYDYLMDYADVMDHPHPEVIHELNRWGVWYTNLTNLDGFRIDAVKH 240
QY 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHSHVFDVPLHYNLNA 300
DB 241 IKYSFTRDMLTHVRNTTGKPMFAVAEFWKNDLGAENYLNKTSWNHSHVFDVPLHYNLNA 300
QY 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
DB 301 SNSGGYYDMRNILNGSVVQKHPHATVTFVNDHDSQPGEALESFVQWFKPLAYALVLTRE 360
QY 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
DB 361 QGYPSVFGDYGYGIPTHGVPAMSKIDPLLOARQTFAYGTQHDYFDHDDIIGWTRGNSS 420
QY 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGWNFNFSVNGGSVS 480
QY 481 VVWKQ 485
DB 481 VVWKQ 485

RESULT 11
US-10-327-837-1
; Sequence 1, Application US/10327837
; Publication No. US20030211958A1
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; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Libbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-7

Query Match 100.0%; Score 2714; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60

Qy 61 YDLYLGEFNOKGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNKHGGADGTEIVNAV 120
Db 61 YDLYLGEFNOKGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNKHGGADGTEIVNAV 120

Qy 121 EVNRSNRNQETSGEYAEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYAEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

Qy 181 RGTGKAWDEVDTEGNYDYLMYADVMDHPEVTHELRNMGVWYTTNTLNDGPRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLMYADVMDHPEVTHELRNMGVWYTTNTLNDGPRIDAVKH 240

Qy 241 IKYSFTDMLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTDMLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300

Qy 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420

Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 13
US-10-184-771-12
; Sequence 12, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Biagard-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18

; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-10-184-771-12

Query Match 100.0%; Score 2714; DB 14; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRDDAANLKSIGITAVWIPPAWKGTSDNDVGGA 60

Qy 61 YDLYLGEFNOKGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNKHGGADGTEIVNAV 120
Db 61 YDLYLGEFNOKGVTRTKYIGTRNQLQAAVTSKNGIQVYGDVVMNKHGGADGTEIVNAV 120

Qy 121 EVNRSNRNQETSGEYAEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180
Db 121 EVNRSNRNQETSGEYAEAWTKFDPGRGNHSSFKRWYHFDGTDQSRQLQNKIYKF 180

Qy 181 RGTGKAWDEVDTEGNYDYLMYADVMDHPEVTHELRNMGVWYTTNTLNDGPRIDAVKH 240
Db 181 RGTGKAWDEVDTEGNYDYLMYADVMDHPEVTHELRNMGVWYTTNTLNDGPRIDAVKH 240

Qy 241 IKYSFTDMLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTDMLTHVNTTCKPMFAVAEFWKNDLGAENYLNKTSWNHVSFVDFVPLHYNLYNA 300

Qy 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMENILNGSVVQKHPHATVFDNHDSPQGEALESFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420
Db 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPLQARQTFAYGTQHDYFDHDDIIGWTREGNSS 420

Qy 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTVTINADGWNFSVNGGSVS 480

Qy 481 VVWKQ 485
Db 481 VVWKQ 485

RESULT 14
US-10-477-725-2
; Sequence 2, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-477-725-2

Query Match 100.0%; Score 2714; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-241;

Matches	485;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	HHNGTNGTMMQYFEWYLPNDGNEHNRRLRDDAANKSGKITAVWI	PPAWKGTSONDVGYGA	60					
Db	1	HHNGTNGTMMQYFEWYLPNDGNEHNRRLRDDAANKSGKITAVWI	PPAWKGTSONDVGYGA	60					
Qy	61	YDLYDLGEFNOQKGTVRTTKYGTNRNQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	120						
Db	61	YDLYDLGEFNOQKGTVRTTKYGTNRNQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	120						
Qy	121	EVNRSNRNQETSGEYAI EAATWKFDPPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180						
Db	121	EVNRSNRNQETSGEYAI EAATWKFDPPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180						
Qy	181	RGTKAWDWEVDTEGNGYDYLMAVDVMDHPHPEVIHELNRWGVYVYTNLTNLDGFRIDAVKH	240						
Db	181	RGTKAWDWEVDTEGNGYDYLMAVDVMDHPHPEVIHELNRWGVYVYTNLTNLDGFRIDAVKH	240						
Qy	241	IKYSFTRDWLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHVSFVDPVPLHYNLYNA	300						
Db	241	IKYSFTRDWLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHVSFVDPVPLHYNLYNA	300						
Qy	301	SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360						
Db	301	SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360						
Qy	361	QGYPSVFYGYGIPTHGVPAKSKIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	420						
Db	361	QGYPSVFYGYGIPTHGVPAKSKIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	420						
Qy	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFVNGSGVS	480						
Db	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFVNGSGVS	480						
Qy	481	VWVKQ 485							
Db	481	VWVKQ 485							

RESULT 15
US-09-986-676A-2
; Sequence 2, Application US/09986676A
; Patent No. US20020102698A1
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: OZAKI, Katsuya
; APPLICANT: ARA, Katsutoshi
; APPLICANT: KAWAI, Shuji
; APPLICANT: ITO, Susumu
; TITLE OF INVENTION: Gene Encoding Alkaline Liquefying Alpha-Amylase
; FILE REFERENCE: 2173-0121P
; CURRENT APPLICATION NUMBER: US/09/986.676A
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/JP96/01641
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: Japan 147257/1995
; PRIOR FILING DATE: 1995-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-986-676A-2

Query Match 96.3%; Score 2613; DB 9; Length 516;
Best Local Similarity 95.1%; Pred. No. 1.2e-231;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;
Qy 1 HHNGTNGTMMQYFEWYLPNDGNEHNRRLRDDAANKSGKITAVWI PPAAWKGTSONDVGYGA 60
Db 32 HHNGTNGTMMQYFEWYLPNDGNEHNRRLRDDAANKSGKITAVWI PPAAWKGTSONDVGYGA 91

Qy	61	YDLYDLGEFNOQKGTVRTTKYGTNRNQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	120
Db	92	YDLYDLGEFNOQKGTVRTTKYGTNRNQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIVNAV	151
Qy	121	EVNRSNRNQETSGEYAI EAATWKFDPPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	180
Db	152	EVNRSNRNQETSGEYTI EAATWKFDPPGRGNHSSFKRWYHFDGTDWDSRQLQNKIYKF	211
Qy	181	RGTKAWDWEVDTEGNGYDYLMAVDVMDHPHPEVIHELNRWGVYVYTNLTNLDGFRIDAVKH	240
Db	212	RGTKAWDWEVDTEGNGYDYLMAVDVMDHPHPEVIHELNRWGVYVYTNLTNLDGFRIDAVKH	271
Qy	241	IKYSFTRDWLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHVSFVDPVPLHYNLYNA	300
Db	272	IKYSFTRDWLTHVRNTTGKPMFAVAEFKNDLGAENYLNKTSWNHVSFVDPVPLHYNLYNA	331
Qy	301	SNSGGYDMRNILNGSVVQKHPTAVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	360
Db	332	SNSGGYDMRNILNGSVVQKHPIHATVTFVDNHDSPQGEALESFVQWFKPLAYALVLTRE	391
Qy	361	QGYPSVFYGYGIPTHGVPAKSKIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	420
Db	392	QGYPSVFYGYGIPTHGVPSMKSIDPLLOARQTFAYGTOHDYFDHDDIIGWTRGNS	451
Qy	421	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFVNGSGVS	480
Db	452	HPNSGLATIMSDGPGGNKMYVGNKAGQVWRDITGNRTGTVTINADGNGFVNGSGVS	511
Qy	481	VWVKQ 485	
Db	512	VWVKQ 516	

Search completed: October 7, 2004, 00:57:24
Job time : 55.4478 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-4

Perfect score: 2720

Sequence: 1 HHNGTNGTMQYFEWHLND.....ADGWANFVNGGVSIVWKR 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2720	100.0	485	2 AAR81836	Aar81836 Bacillus
2	2720	100.0	485	2 AAW31500	Aaw31500 Bacillus
3	2720	100.0	485	2 AAW48261	Aaw48261 Bacillus
4	2720	100.0	485	2 AAY15422	Aay15422 Termamyl-1
5	2720	100.0	485	2 AAY15416	Aay15416 Bacillus
6	2720	100.0	485	2 AAY07382	Aay07382 Wild type
7	2720	100.0	485	3 AAY99609	Aay99609 Bacillus
8	2720	100.0	485	3 AAY99603	Aay99603 Bacillus
9	2720	100.0	485	5 ABB06934	Abb06934 Bacillus
10	2720	100.0	485	5 AAU12150	Aau12150 Bacillus
11	2720	100.0	485	5 AAB47851	Aab47851 Bacillus
12	2720	100.0	485	5 ABB76587	Abb76587 Termamyl-1
13	2720	100.0	485	6 ABB99481	Abb99481 Amino aci
14	2720	100.0	834	4 AAB30701	Aab30701 A Bacillu
15	2712	99.7	485	2 AAY07392	Aay07392 Wild type
16	2709	99.6	485	5 ABB76636	Abb76636 Termamyl-1
17	2708	99.6	485	5 ABB76639	Abb76639 Termamyl-1
18	2707	99.5	485	2 AAY25151	Aay25151 Bacillus
19	2706	99.5	485	5 ABB76637	Abb76637 Termamyl-1
20	2705	99.4	485	5 ABB76643	Abb76643 Termamyl-1
21	2703	99.4	485	5 ABB76640	Abb76640 Termamyl-1
22	2701	99.3	485	5 ABB76644	Abb76644 Termamyl-1
23	2701	99.3	485	5 ABB76641	Abb76641 Termamyl-1
24	2701	99.3	485	5 ABB76642	Abb76642 Termamyl-1
25	2698	99.2	483	2 AAW12139	Aaw12139 Alpha-amy

26	2698	99.2	485	5 ABB76638	Abb76638 Termamyl-1
27	2697	99.2	483	2 AAW12137	Aaw12137 Alpha-amy
28	2697	99.2	483	2 AAY13444	Aay13444 Alpha-amy
29	2692	99.0	481	4 ABB00011	Abb00011 Bacillus
30	2691	98.9	483	2 AAW12138	Aaw12138 Alpha-amy
31	2691	98.9	483	2 AAW12140	Aaw12140 Alpha-amy
32	2690	98.9	483	2 AAW12143	Aaw12143 Alpha-amy
33	2457	90.3	485	2 AAW12110	Aaw12110 Alpha-amy
34	2455	90.3	485	2 AAW12144	Aaw12144 Alpha-amy
35	2454	90.2	485	2 AAW12109	Aaw12109 Alpha-amy
36	2448	90.0	485	2 AAW31499	Aaw31499 Bacillus
37	2448	90.0	485	2 AAW48260	Aaw48260 Bacillus
38	2448	90.0	485	2 AAY15421	Aay15421 Termamyl-1
39	2448	90.0	485	2 AAY15415	Aay15415 Bacillus
40	2448	90.0	485	2 AAY25150	Aay25150 Bacillus
41	2448	90.0	485	2 AAY07391	Aay07391 Wild type
42	2448	90.0	485	2 AAY07381	Aay07381 Wild type
43	2448	90.0	485	3 AAY99602	Aay99602 Bacillus
44	2448	90.0	485	3 AAY99608	Aay99608 Bacillus
45	2448	90.0	485	5 ABB06933	Abb06933 Bacillus

ALIGNMENTS

RESULT 1

AAR81836
ID AAR81836 standard; protein; 485 AA.

XX AAR81836;

DT 16-MAR-1996 (first entry)

DE Bacillus sp. alkaline alpha-amylase.

XX Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile; beer; starch.

OS Bacillus.

PN W09526397-A1.

XX 05-OCT-1995.

PF 29-MAR-1995; 95WO-DK000142.

PR 29-MAR-1994; 94DK-00000353.

PR 03-NOV-1994; 94DK-00001271.

PR 03-FEB-1995; 95DK-00000123.

XX (NOVO) NOVO-NORDISK AS.

PI Outtrup H, Bisgard-Frantzen H, Ostergaard PR, Rasmussen MD;

XX Van Der Zee P;

DR WPI; 1995-351318/45.

XX N-PSDB; AAT00777.

FT New alkaline Bacillus alpha-amylase - used in e.g. detergent compans.

XX starch liquefaction, textile desizing, starch modification or beer making.

PS Claim 5; Page 46-48; 65pp; English.

XX This alpha-amylase protein is characterized by having a specific activity at least 25% higher than the specific activity of Termamyl at 25-55 deg C and a pH of 8-10. The enzyme can be used in detergent composition for starch liquefaction, the production of lignocellulosic materials, e.g. pulp, paper and cardboard from waste containing starch, for deinking recycled starch-coated, or starch- containing printed paper, to modify starch for papermaking, for textile desizing, and beer-making processes. This protein may be produced recombinantly

SQ	Sequence 485 AA;	
PT	Query Match	100.0%; Score 2720; DB 2; Length 485;
PT	Best Local Similarity	100.0%; Pred. No. 3.2e-212;
XX	Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PS	Claim 1; Page 88-89; 97pp; English.	
XX	The present sequence is a Bacillus sp. alpha amylase with a specific activity at least 25% higher than that of Termamyl (RTM) at 25 to 55 degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It is of use in hard surface cleaning, hand or machine dishwashing and laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain removal and fabric care are obtained by using it at a concentration of 0.00018 to 0.08%	
XX	Sequence 485 AA;	
SQ	Query Match	100.0%; Score 2720; DB 2; Length 485;
PT	Best Local Similarity	100.0%; Pred. No. 3.2e-212;
XX	Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 HNGTNGTMMQYFEWHLPNDSNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60	
DB	1 HNGTNGTMMQYFEWHLPNDSNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60	
QY	61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVYGDVVMNHKGGADATENVLAV 120	
DB	61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVYGDVVMNHKGGADATENVLAV 120	
QY	121 EVNPNRNRQEIISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFQNRIFYK 180	
DB	121 EVNPNRNRQEIISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFQNRIFYK 180	
QY	181 RGDGKAWDEVDSENGNYDILMYADVMDHPVNNELRRWGEWYTTNLNLDGFRIDAVKH 240	
DB	181 RGDGKAWDEVDSENGNYDILMYADVMDHPVNNELRRWGEWYTTNLNLDGFRIDAVKH 240	
QY	241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNQDLGALENYLNKTNWNHVSFVDPVPLHYNLYNA 300	
DB	241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNQDLGALENYLNKTNWNHVSFVDPVPLHYNLYNA 300	
QY	301 SNSGGNYDMAKLLNGTVVQKHPMHAFTFVDNHDSDQGESLESFVQEWFKPLAYALILTRE 360	
DB	301 SNSGGNYDMAKLLNGTVVQKHPMHAFTFVDNHDSDQGESLESFVQEWFKPLAYALILTRE 360	
QY	361 QGYPSVFYGDYIGIPTHSPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420	
DB	361 QGYPSVFYGDYIGIPTHSPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420	
QY	421 HPNSGLATIMSDGPGGKMWYGVQNKAGQVWHDIITGNKPGTGTVTINADGWANFVSNGGSVS 480	
DB	421 HPNSGLATIMSDGPGGKMWYGVQNKAGQVWHDIITGNKPGTGTVTINADGWANFVSNGGSVS 480	
QY	481 IWVKR 485	
DB	481 IWVKR 485	
XX	AAW31500; standard; protein; 485 AA.	
XX	AAW31500;	
XX	08-APR-1998 (first entry)	
XX	Bacillus sp. alpha amylase.	
XX	Alpha amylase; hard surface cleaning; dishwashing; laundry.	
XX	Bacillus sp.	
XX	WO9732961-A2.	
XX	12-SEP-1997.	
XX	04-MAR-1997; 97WO-US003635.	
XX	07-MAR-1996; 96WO-US003276.	
XX	(PROC) PROCTER & GAMBLE CO.	
XX	Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;	
XX	Ward G;	
XX	WPI; 1997-457524/42.	
XX	Detergent compositions for hard surface cleaning and laundry use -	

PT	contains Bacillus derived alpha amylase with improved thermostability, reduced calcium ion dependency etc.	
PS	Claim 1; Page 88-89; 97pp; English.	
XX	The present sequence is a Bacillus sp. alpha amylase with a specific activity at least 25% higher than that of Termamyl (RTM) at 25 to 55 degrees C at pH 8 to 10, measured by the Phadebas (RTM) activity test. It is of use in hard surface cleaning, hand or machine dishwashing and laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain removal and fabric care are obtained by using it at a concentration of 0.00018 to 0.08%	
XX	Sequence 485 AA;	
SQ	Query Match	100.0%; Score 2720; DB 2; Length 485;
PT	Best Local Similarity	100.0%; Pred. No. 3.2e-212;
XX	Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 HNGTNGTMMQYFEWHLPNDSNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60	
DB	1 HNGTNGTMMQYFEWHLPNDSNHNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60	
QY	61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVYGDVVMNHKGGADATENVLAV 120	
DB	61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVYGDVVMNHKGGADATENVLAV 120	
QY	121 EVNPNRNRQEIISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFQNRIFYK 180	
DB	121 EVNPNRNRQEIISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFQNRIFYK 180	
QY	181 RGDGKAWDEVDSENGNYDILMYADVMDHPVNNELRRWGEWYTTNLNLDGFRIDAVKH 240	
DB	181 RGDGKAWDEVDSENGNYDILMYADVMDHPVNNELRRWGEWYTTNLNLDGFRIDAVKH 240	
QY	241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNQDLGALENYLNKTNWNHVSFVDPVPLHYNLYNA 300	
DB	241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNQDLGALENYLNKTNWNHVSFVDPVPLHYNLYNA 300	
QY	301 SNSGGNYDMAKLLNGTVVQKHPMHAFTFVDNHDSDQGESLESFVQEWFKPLAYALILTRE 360	
DB	301 SNSGGNYDMAKLLNGTVVQKHPMHAFTFVDNHDSDQGESLESFVQEWFKPLAYALILTRE 360	
QY	361 QGYPSVFYGDYIGIPTHSPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420	
DB	361 QGYPSVFYGDYIGIPTHSPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420	
QY	421 HPNSGLATIMSDGPGGKMWYGVQNKAGQVWHDIITGNKPGTGTVTINADGWANFVSNGGSVS 480	
DB	421 HPNSGLATIMSDGPGGKMWYGVQNKAGQVWHDIITGNKPGTGTVTINADGWANFVSNGGSVS 480	
QY	481 IWVKR 485	
DB	481 IWVKR 485	
XX	AAW48261 standard; protein; 485 AA.	
XX	AAW48261;	
XX	02-JUL-1998 (first entry)	
XX	Bacillus sp. alpha amylase protein #2.	
XX	Alpha amylase; stain digestion; detergent; fabric laundry performance.	
XX	Bacillus sp.	
XX	WO9805748-A1.	
XX	12-FEB-1998.	

XX 01-AUG-1996; 96WO-US012612.
 XX 01-AUG-1996; 96WO-US012612.
 XX (PROC) PROCTER & GAMBLE CO.
 XX Baek AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;
 XX WPI; 1998-159168/14.
 XX Use of specific alpha-amylase enzymes - in laundry detergent compositions
 XX to provide effective cleaning and whitening of dingy fabrics.
 XX Claim 1; Page 71-72; 82pp; English.
 XX This sequence represents an alpha amylase from Bacillus sp. which is used
 XX in a laundry detergent. The detergent compositions can be used for
 XX boosting fabric laundry performance or for dingy fabric cleanup
 XX Sequence 485 AA;
 Query Match 100.0%; Score 2720; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGGA 60
 DB 1 HHNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGGA 60
 QY 61 YDLYDLGEFNOGKGTVRTKYGTRSOLESAIHALKNGGVQVYGVVNMHKGADATENVLAV 120
 DB 61 YDLYDLGEFNOGKGTVRTKYGTRSOLESAIHALKNGGVQVYGVVNMHKGADATENVLAV 120
 QY 121 EVNPNRNRQETISGDYTTIEAWTKFDPGKGTNTYDFKRWYHFGVDVQSRQFQNRYYKF 180
 DB 121 EVNPNRNRQETISGDYTTIEAWTKFDPGKGTNTYDFKRWYHFGVDVQSRQFQNRYYKF 180
 QY 181 RGDGKAWDWEVDSNGNYDYLMDVADVMDHDPVNVNLRNGEWYTNLNDGFRIDAVKH 240
 DB 181 RGDGKAWDWEVDSNGNYDYLMDVADVMDHDPVNVNLRNGEWYTNLNDGFRIDAVKH 240
 QY 241 IKYSFTRDLWTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
 DB 241 IKYSFTRDLWTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
 QY 301 SNSSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 DB 301 SNSSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 QY 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420
 DB 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420
 QY 481 IWVKR 485
 DB 481 IWVKR 485
 RESULT 4
 AAY15422
 ID AAY15422 standard; protein; 485 AA.
 XX AC
 XX AAY15422;
 XX AC
 XX 22-JUL-1999 (first entry)
 XX DE
 XX Termamyl-like alpha-amylase protein.

KW Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 KW saccharification process.
 OS Bacillus sp.
 PN WO99232211-A1.
 XX 14-MAY-1999.
 XX 30-OCT-1998; 98WO-DK000471.
 XX 30-OCT-1997; 97DK-00001240.
 PR 14-JUL-1998; 98DK-00000936.
 XX (NOVO) NOVO-NORDISK AS.
 XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
 PI Kjaerulff S;
 XX WPI; 1999-326987/27.
 XX New Termamyl-like alpha-amylase variants.
 PS Claim 38; Page 89-91; 115pp; English.
 XX The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
 CC D144, F145, P146, G147, G149, G174, R181, G182, D183, G184, K185,
 CC A186, W189, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
 CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
 CC K311, E346, K385, G456, N457, K458, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention
 XX Sequence 485 AA;
 Query Match 100.0%; Score 2720; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGGA 60
 DB 1 HHNGTNGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGGA 60
 QY 61 YDLYDLGEFNOGKGTVRTKYGTRSOLESAIHALKNGGVQVYGVVNMHKGADATENVLAV 120
 DB 61 YDLYDLGEFNOGKGTVRTKYGTRSOLESAIHALKNGGVQVYGVVNMHKGADATENVLAV 120
 QY 121 EVNPNRNRQETISGDYTTIEAWTKFDPGKGTNTYDFKRWYHFGVDVQSRQFQNRYYKF 180
 DB 121 EVNPNRNRQETISGDYTTIEAWTKFDPGKGTNTYDFKRWYHFGVDVQSRQFQNRYYKF 180
 QY 181 RGDGKAWDWEVDSNGNYDYLMDVADVMDHDPVNVNLRNGEWYTNLNDGFRIDAVKH 240
 DB 181 RGDGKAWDWEVDSNGNYDYLMDVADVMDHDPVNVNLRNGEWYTNLNDGFRIDAVKH 240
 QY 241 IKYSFTRDLWTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
 DB 241 IKYSFTRDLWTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
 QY 301 SNSSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 DB 301 SNSSGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 QY 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420
 DB 361 QGYPSVFYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420

QY 421 HPSGLATIMSDGPGGKMYVGNKAGQVWHDTGNKPGTGTINADGWANFVNGGSVS 480
DB 421 HPSGLATIMSDGPGGKMYVGNKAGQVWHDTGNKPGTGTINADGWANFVNGGSVS 480

QY 481 IWVKR 485
DB 481 IWVKR 485

RESULT 5
ID AAY15416 standard; protein; 485 AA.
AC AAY15416;
XX
DT 22-JUL-1999 (first entry)
DE Bacillus alpha-amylase protein.
XX
KW Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
KW saccharification process.
XX
OS Bacillus sp.
XX
PN WO9923211-A1.
XX
PD 14-MAY-1999.
XX
PF 30-OCT-1998; 98WO-DK000471.
XX
PR 30-OCT-1997; 97DK-00001240.
PR 14-JUL-1998; 98DK-0000936.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
PI Kjaerulff S;
XX
DR WPI; 1998-326987/27.
XX
PT New Termamyl-like alpha-amylase variants.
PS Claim 38; Page 79-80; 115pp; English.
XX
CC The specification describes termamyl-like alpha-amylase variants that
CC have altered amino acid sequences to improve properties. The variants are
CC produced by creating one or more of the following mutations in amino acid
CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
CC L171, Q172, F173, F267, W268, K269, N270, D271, L272, A274, L275,
CC K311, E346, K385, G456, K457, K458, N459, G460, T461, V462, T463. The
CC variants can be used for washing and/or dishwashing. They can also be
CC used in the production of sweeteners and ethanol from starch, and/or for
CC textile desizing, and in starch liquefaction and/or saccharification
CC processes. The present amylase can function as the parent sequence in the
CC production of the variants of the invention
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPNQDNHNRRLRDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWHLPNQDNHNRRLRDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60

QY 61 YDLVGLGEFNKQGTVRTKYGTRSOLESAIHALKNNGVQVYGVVMMHKGADATENVLAV 120
DB 61 YDLVGLGEFNKQGTVRTKYGTRSOLESAIHALKNNGVQVYGVVMMHKGADATENVLAV 120

QY 121 EVNPNRNOEISGDIYIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSQRFQNRYYKF 180
DB 121 EVNPNRNOEISGDIYIEAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSQRFQNRYYKF 180

QY 181 RGDGKAWDEVDSENGNYDYLAMYADVMDHPHPEVNNELRWGEWYTTNLDGFRIDAVKH 240
DB 181 RGDGKAWDEVDSENGNYDYLAMYADVMDHPHPEVNNELRWGEWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENYLNKTNWNHVSFDPVPLHYNLNA 300
DB 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENYLNKTNWNHVSFDPVPLHYNLNA 300

QY 301 SNSGGNYDMAKLNGTVVQKHPMHAVTFVDNHDSDQFSGESLEFVQWFKPLAYALILTRE 360
DB 301 SNSGGNYDMAKLNGTVVQKHPMHAVTFVDNHDSDQFSGESLEFVQWFKPLAYALILTRE 360

QY 361 QGYPSVFGDYGYGIPTHSVPAKAKIDPILARPONFAYGTQHDYFDHNNIIGWTREGNTT 420
DB 361 QGYPSVFGDYGYGIPTHSVPAKAKIDPILARPONFAYGTQHDYFDHNNIIGWTREGNTT 420

QY 421 HPSGLATIMSDGPGGKMYVGNKAGQVWHDTGNKPGTGTINADGWANFVNGGSVS 480
DB 421 HPSGLATIMSDGPGGKMYVGNKAGQVWHDTGNKPGTGTINADGWANFVNGGSVS 480

QY 481 IWVKR 485
DB 481 IWVKR 485

RESULT 6
ID AAY07382 standard; protein; 485 AA.
XX
AC AAY07382;
XX
DT 16-JUL-1999 (first entry)
DE Wild type Termamyl (RTM)-like alpha-amylase protein #2.
XX
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
KW ethanol.
XX
OS Bacillus sp.
XX
PH Key Location/Qualifiers
FT Misc-difference 181..184
FT /note= "optionally 1, 2, 3 or all residues are deleted"
FT Misc-difference 195
FT /note= "optionally altered to any amino acid except an
FT Asn residue"
FT Misc-difference 206
FT /note= "optionally altered to any amino acid except a Val
FT residue"
FT Misc-difference 212
FT /note= "optionally altered to any amino acid except a Glu
FT residue"
FT Misc-difference 216
FT /note= "optionally altered to any amino acid except a Glu
FT residue"
FT Misc-difference 269
FT /note= "optionally altered to any amino acid except a Lys
FT residue"
XX
PN WO9919467-A1.
XX
PD 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK000444.
XX
PR 13-OCT-1997; 97DK-00001172.
XX

```
PA (NOVO ) NOVO-NORDISK AS.
XX
XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
PI Svendsen A, Borchert TV, Bisgard-Frantzen H;
XX
XX WPI; 1999-277632/23.
XX
XX Variant alpha-amylases - useful as detergents or for textile desizing or
PT starch liquefaction.
XX
XX Claim 1; Page 63-65; 93pp; English.
XX
XX This sequence represents the parent sequence for new variants of a parent
CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants
CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
CC from either of two Bacillus species in WO9526397, B. stearothermophilus,
CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
CC amylase variants are detergent additives for use in detergents for
CC dishwashing, manual or automatic laundry. The variants can also be used
CC for textile desizing or starch liquefaction (e.g. for production of
CC sweeteners or ethanol)
XX
XX Sequence 485 AA;
SQ
Query Match 100.0%; Score 2720; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHNGTGTMMQYFEWHLFNDGNHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWHLFNDGNHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
QY 61 YDLVLDLGEFQKQGVTRTKYGRSQAIAHALKKNQGVQVYGDVVMNKHGGADATENVLAV 120
DB 61 YDLVLDLGEFQKQGVTRTKYGRSQAIAHALKKNQGVQVYGDVVMNKHGGADATENVLAV 120
QY 121 EVNPNRNRQEISGDTTTEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQDSQFQNRKYKF 180
DB 121 EVNPNRNRQEISGDTTTEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQDSQFQNRKYKF 180
QY 181 RGDGKAWDWEVDSENGNYDYLMAVDMDHPEVNVNLRNGEWYTNLTLDGFRIDAVKH 240
DB 181 RGDGKAWDWEVDSENGNYDYLMAVDMDHPEVNVNLRNGEWYTNLTLDGFRIDAVKH 240
QY 241 IKYSFTEDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300
DB 241 IKYSFTEDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300
QY 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILITRE 360
DB 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILITRE 360
QY 361 QGYPVSFYGDYIGPTHSVPAMKAKIDPILBARONFAYGTOHDYFDHNNIIGWTREGNTT 420
DB 361 QGYPVSFYGDYIGPTHSVPAMKAKIDPILBARONFAYGTOHDYFDHNNIIGWTREGNTT 420
QY 421 HPNSGLATIMSDGPGGKMWYVGNKAGVQVWHDTGNKPGVTITNADGANFVSNGGSVS 480
DB 421 HPNSGLATIMSDGPGGKMWYVGNKAGVQVWHDTGNKPGVTITNADGANFVSNGGSVS 480
QY 481 IWVKR 485
DB 481 IWVKR 485
RESULT 7
ID AAY99609
XX AAY99609 standard; protein; 485 AA.
AC AAY99609;
XX
XX 04-SEP-2000 (first entry)
XX
XX Bacillus Termamyl-like alpha-amylase #4.
DE
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XX
XX Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; mutein; mutant; enzyme stability; hybrid.
XX
XX Bacillus sp.
XX
XX WO200029560-A1.
XX
XX 25-MAY-2000.
XX
XX 16-NOV-1999; 99WO-DK000628.
XX
XX 16-NOV-1998; 98DK-00001495.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
XX
XX WPI; 2000-387777/33.
XX
XX Variant of parent termamyl-like alpha amylase useful for washing, textile
PT desizing and starch liquefaction, comprising alterations in one or more
PT solvent exposed amino acid residues.
XX
XX Claim 8; Page 64-65; 80pp; English.
XX
XX The present sequence is a parent alpha-amylase from which mutants with
CC increased stability at acidic pH, low calcium concentration and high
CC temperatures have been derived. The sequence encoding this enzyme was
CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of methyl
CC groups in the side chains of exposed residues may be increased. The
CC mutations can be incorporated by site-directed mutagenesis or by random
CC mutagenesis. As a result of their increased stability, the variants are
CC suitable for the industrial processing of starch, i.e. starch
CC liquefaction and saccharification. They may also be useful for washing,
CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
CC partial amino acid sequences derived from two or more alpha-amylases have
CC also been created in order to increase enzyme stability
XX
XX Sequence 485 AA;
SQ
Query Match 100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.2e-212;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHNGTGTMMQYFEWHLFNDGNHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWHLFNDGNHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
QY 61 YDLVLDLGEFQKQGVTRTKYGRSQAIAHALKKNQGVQVYGDVVMNKHGGADATENVLAV 120
DB 61 YDLVLDLGEFQKQGVTRTKYGRSQAIAHALKKNQGVQVYGDVVMNKHGGADATENVLAV 120
QY 121 EVNPNRNRQEISGDTTTEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQDSQFQNRKYKF 180
DB 121 EVNPNRNRQEISGDTTTEAWTKFDFPGRGNTYSDFKRWYHFDGVDWQDSQFQNRKYKF 180
QY 181 RGDGKAWDWEVDSENGNYDYLMAVDMDHPEVNVNLRNGEWYTNLTLDGFRIDAVKH 240
DB 181 RGDGKAWDWEVDSENGNYDYLMAVDMDHPEVNVNLRNGEWYTNLTLDGFRIDAVKH 240
QY 241 IKYSFTEDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300
DB 241 IKYSFTEDLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300
QY 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILITRE 360
DB 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILITRE 360
QY 361 QGYPVSFYGDYIGPTHSVPAMKAKIDPILBARONFAYGTOHDYFDHNNIIGWTREGNTT 420
DB 361 QGYPVSFYGDYIGPTHSVPAMKAKIDPILBARONFAYGTOHDYFDHNNIIGWTREGNTT 420
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Db 361 QGYPSVFYGDYYGIPTHSVPMKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 QY 421 HPNSGLATIMSDGPGGKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGSVS 480
 Db 421 HPNSGLATIMSDGPGGKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGSVS 480
 QY 481 IWVKR 485
 Db 481 IWVKR 485

RESULT 8
 AAY99603
 ID AAY99603 standard; protein; 485 AA.
 AC AAY99603;
 XX
 XX
 DT 04-SEP-2000 (first entry)
 DE Bacillus parent Termamyl-like alpha-amylase #2.
 XX
 XX
 KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 KW saccharification; mutein; mutant; enzyme stability; hybrid.
 XX
 OS Bacillus sp.
 XX
 XX WO200029560-A1.
 PN
 XX
 XX 25-MAY-2000.
 XX
 PF 16-NOV-1999; 99WO-DK000628.
 XX
 PR 16-NOV-1998; 98DK-00001495.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX
 PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
 XX
 DR WPI: 2000-38777/33.
 DR N-PSDB; AAA48482.
 XX
 XX Variant of parent termamyl-like alpha amylase useful for washing, textile
 PT desizing and starch liquefaction, comprising alterations in one or more
 PT solvent exposed amino acid residues.
 XX
 XX Claim 8; Page 54-56; 80pp; English.
 XX
 XX The present sequence is a parent Termamyl-like alpha-amylase from which
 CC mutants with increased stability at acidic pH, low calcium concentration
 CC and high temperatures have been derived. The sequence encoding this
 CC enzyme was isolated from a Bacillus genomic DNA library. A variant may
 CC contain mutations in one or more solvent exposed amino acid residues to
 CC increase the overall hydrophobicity of the enzyme or the overall number
 CC of methyl groups in the side chains of exposed residues may be increased.
 CC The mutations can be incorporated by site-directed mutagenesis or by
 CC random mutagenesis. As a result of their increased stability, the
 CC variants are suitable for the industrial processing of starch, i.e.
 CC starch liquefaction and saccharification. They may also be useful for
 CC washing, dishwashing and textile desizing. Hybrid alpha-amylases
 CC comprising partial amino acid sequences derived from two or more alpha-
 CC amylases have also been created in order to increase enzyme stability
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 3; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNDDGNHNRRLDDASNLNRNGITAIWTPPAWKGTQNDVGYGA 60
 Db 1 HHNGTNGTMMQYFEWHLPNDDGNHNRRLDDASNLNRNGITAIWTPPAWKGTQNDVGYGA 60
 QY 61 YDLYDLGEFNGKGTVRTKYTRSQLESIAHALKNNGVQYVGVMMHKGADATENVLAV 120

Db 61 YDLYDLGEFNGKGTVRTKYTRSQLESIAHALKNNGVQYVGVMMHKGADATENVLAV 120
 QY 121 EVNPNRNQIEISGDYITIAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSRQFQNIYKF 180
 Db 121 EVNPNRNQIEISGDYITIAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSRQFQNIYKF 180
 QY 181 RGDGKAWDEVDSENGNYDLYADVMDHPPEVNMELRWGSEWYNTNLDGFRIDAVKH 240
 Db 181 RGDGKAWDEVDSENGNYDLYADVMDHPPEVNMELRWGSEWYNTNLDGFRIDAVKH 240
 QY 241 IKYSFTTRDLTHVRNATGKEMFAVEFWKNDLGALENYLKNTNWNHVSFVDPVPLHYNLYNA 300
 Db 241 IKYSFTTRDLTHVRNATGKEMFAVEFWKNDLGALENYLKNTNWNHVSFVDPVPLHYNLYNA 300
 QY 301 SNSGGNYDMAKLLNGTIVQKHPHVAFTVDNHDSDPGESLESFVQWFKPLAYALILTRE 360
 Db 301 SNSGGNYDMAKLLNGTIVQKHPHVAFTVDNHDSDPGESLESFVQWFKPLAYALILTRE 360
 QY 361 QGYPSVFYGDYYGIPTHSVPMKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 Db 361 QGYPSVFYGDYYGIPTHSVPMKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 QY 421 HPNSGLATIMSDGPGGKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGSVS 480
 Db 421 HPNSGLATIMSDGPGGKMYVQNKAGOVHDDITGNKPGTVTINADGWANFVNGSVS 480
 QY 481 IWVKR 485
 Db 481 IWVKR 485

RESULT 9
 ABB06934
 ID ABB06934 standard; protein; 485 AA.
 AC ABB06934;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:4.
 XX
 KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX
 OS Bacillus sp.
 XX
 XX WO200166712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-0000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 XX (NOVO) NOVOZYMES AS.
 PA
 XX
 PI Andersen C, Borchert TV, Nielsen BR;
 XX
 DR WPI; 2002-239612/29.
 DR N-PSDB; ABL50565.
 XX
 XX Novel variant of parent termamyl-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 135-136; 153pp; English.
 XX
 CC The present invention describes a variant of a parent termamyl-like alpha

CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg182, Gly184, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a *Bacillus* termamyl-like alpha-amylase which
 CC is used in the exemplification of the present invention

XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIIPPAWKGTQNDVGYGA 60
 DB 1 HNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIIPPAWKGTQNDVGYGA 60
 QY 61 YDYLDFGEFQKGTVRTKYTRSQLESIAIHALKNGVQVYGVVNMHKGADATENVLAV 120
 DB 61 YDYLDFGEFQKGTVRTKYTRSQLESIAIHALKNGVQVYGVVNMHKGADATENVLAV 120
 QY 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSRQFNRIYKF 180
 DB 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSRQFNRIYKF 180
 QY 181 RGDGKAWDEVDSENGNYDLYMADVMDHPEVNNELRRGWYNTNLNLDGFRIDAVKH 240
 DB 181 RGDGKAWDEVDSENGNYDLYMADVMDHPEVNNELRRGWYNTNLNLDGFRIDAVKH 240
 QY 241 IKYSFTRDMLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWNSHVSFVDFPLHNLNYA 300
 DB 241 IKYSFTRDMLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWNSHVSFVDFPLHNLNYA 300
 QY 301 SNSSGNYDMAKLLNGTIVVQKHPHMAVTFVDNHDHDSQGESLESFVQEWFKPLAYALILTRE 360
 DB 301 SNSSGNYDMAKLLNGTIVVQKHPHMAVTFVDNHDHDSQGESLESFVQEWFKPLAYALILTRE 360
 QY 361 QGYPSPFYGYDYGIPHTSHVPAMKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 DB 361 QGYPSPFYGYDYGIPHTSHVPAMKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 QY 421 HPNSGLATIMSDGPGGKEMMYVGONKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480
 DB 421 HPNSGLATIMSDGPGGKEMMYVGONKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480
 QY 481 IWVKR 485
 DB 481 IWVKR 485

RESULT 10

AAU12150

ID AAU12150 standard; protein; 485 AA.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

PN W0200188107-A2.

XX 22-NOV-2001.

XX 10-MAY-2001; 2001WO-DK000323.

XX 12-MAY-2000; 2000DK-00000779.

XX (NOVO) NOVOZYMES AS.

XX Svendsen A, Jorgensen CT, Nielsen BR;

XX WPI; 2002-106123/14.

XX N-PSDB; AAS20023.

XX New variant of parent Termamyl-like alpha-amylase for use as a component

XX in washing and dishwashing compositions, for textile desizing, for starch

XX liquefaction, and for producing sweeteners and ethanol from starch.

XX Claim 5; Fig 1; 84pp; English.

XX The invention relates to a variant of parent TERMAMYL-like alpha- amylase

XX comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,

XX or at position 234, where the variant has alpha-amylase activity and each

XX position corresponds to a position of a parent termamyl-like alpha-

XX amylase sequence having a *Bacillus* licheniformis alpha-amylase sequence

XX of 483 amino acids, given in specification. The variant alpha- amylase, a

XX detergent additive comprising the variant or a detergent composition

XX comprising the variant, is useful for washing and/or dishwashing or

XX textile desizing. The alpha-amylase is useful for starch liquefaction or

XX ethanol production and as a component in a hard surface cleaning

XX detergent composition, and for producing sweeteners from starch. The

XX variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage

XX activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic

XX branch linkage cleavage activity of amylopectin or a limit dextrin

XX prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a

XX natural variant of the TERMAMYL alpha-amylase, SP722

XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 5; Length 485;

Best Local Similarity 100.0%; Pred. No. 3.2e-212;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIIPPAWKGTQNDVGYGA 60

DB 1 HNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIIPPAWKGTQNDVGYGA 60

QY 61 YDYLDFGEFQKGTVRTKYTRSQLESIAIHALKNGVQVYGVVNMHKGADATENVLAV 120

DB 61 YDYLDFGEFQKGTVRTKYTRSQLESIAIHALKNGVQVYGVVNMHKGADATENVLAV 120

QY 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSRQFNRIYKF 180

DB 121 EVNPNRNRQISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVDWDQSRQFNRIYKF 180

QY 181 RGDGKAWDEVDSENGNYDLYMADVMDHPEVNNELRRGWYNTNLNLDGFRIDAVKH 240

DB 181 RGDGKAWDEVDSENGNYDLYMADVMDHPEVNNELRRGWYNTNLNLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWNSHVSFVDFPLHNLNYA 300

DB 241 IKYSFTRDMLTHVRNATGKEMFAVAEFKNDLGALENYLNKTNWNSHVSFVDFPLHNLNYA 300

QY 301 SNSSGNYDMAKLLNGTIVVQKHPHMAVTFVDNHDHDSQGESLESFVQEWFKPLAYALILTRE 360

DB 301 SNSSGNYDMAKLLNGTIVVQKHPHMAVTFVDNHDHDSQGESLESFVQEWFKPLAYALILTRE 360

QY 361 QGYPSPFYGYDYGIPHTSHVPAMKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420

DB 361 QGYPSPFYGYDYGIPHTSHVPAMKAKIDPILKARQNFAYGTQHDYFDHNNIIGWTREGNTT 420

QY 421 HPNSGLATIMSDGPGGKEMMYVGONKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480

DB 421 HPNSGLATIMSDGPGGKEMMYVGONKAGQVWHDTITGNKPGTIVTINADGWANFVSNGGSVS 480

QY 481 IWVKR 485

DB 481 IWVKR 485

Db 421 HPSGLATIMSDGPGGKMYVGONKAGQVWHDTGNKPGTVTINADGWANFVNGGSVS 480
 QY 481 IWVCR 485
 Db 481 IWVCR 485

RESULT 11
 AAB47851
 ID AAB47851 standard; protein; 485 AA.
 AC AAB47851;
 DT 02-APR-2002 (first entry)
 XX Bacillus alpha amylase sp722.
 DE Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KW cured meat; fermented meat; spice.
 XX Bacillus sp.
 XX WO200196537-A2.
 XX 20-DEC-2001.
 XX 13-JUN-2001; 2001WO-DK000404.
 XX 14-JUN-2000; 2000DK-00000917.
 XX 20-JUN-2000; 2000US-0212852P.
 XX (NOVO) NOVOZYMES AS.
 XX Nielsen BR, Weibye M;
 XX WPI; 2002-098064/13.
 XX N-PSDB; AAI72212.
 XX New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX Claim 5; Page 28-30; 47pp; English.
 XX The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kda has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX Sequence 485 AA;
 SQ

Query Match 100.0%; Score 2720; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HNGTGTMMQYFEWHLPGNDGNHNRLLRDDASLNRRGITAIIWIPPAWKTSQNDVGGA 60
 Db 1 HNGTGTMMQYFEWHLPGNDGNHNRLLRDDASLNRRGITAIIWIPPAWKTSQNDVGGA 60

QY 61 YDIYDLGEFNOKGTVTYTKYTRSQLESATHALKNGGVQVYGVVMMHKGADATENVLAV 120
 Db 61 YDIYDLGEFNOKGTVTYTKYTRSQLESATHALKNGGVQVYGVVMMHKGADATENVLAV 120
 QY 121 EVNPNRNRNOEISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFQNRYYKF 180
 Db 121 EVNPNRNRNOEISGDYTIETAWTKFDFPGRGNTYSDFKRWYHFDGVWDQSRQFQNRYYKF 180
 QY 181 RGDGKAWDEVDSENGNYDLYMYADVMDHPEVYNELRRGWGYTNTLNDGFRIDAVKH 240
 Db 181 RGDGKAWDEVDSENGNYDLYMYADVMDHPEVYNELRRGWGYTNTLNDGFRIDAVKH 240
 QY 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNLDGALENYLNKTWNHNSVDPVPLHYNLYNA 300
 Db 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNLDGALENYLNKTWNHNSVDPVPLHYNLYNA 300
 QY 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSDQGESLESFVQWFKPLAYALLITRE 360
 Db 301 SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSDQGESLESFVQWFKPLAYALLITRE 360
 QY 361 QGYPSVFGDYGYGIPHTSPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 Db 361 QGYPSVFGDYGYGIPHTSPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 QY 421 HNSGLATIMSDGPGGKMYVGONKAGQVWHDTGNKPGTVTINADGWANFVNGGSVS 480
 Db 421 HNSGLATIMSDGPGGKMYVGONKAGQVWHDTGNKPGTVTINADGWANFVNGGSVS 480
 QY 481 IWVCR 485
 Db 481 IWVCR 485

RESULT 12
 ABB76587
 ID ABB76587 standard; protein; 485 AA.
 XX ABB76587;
 DT 19-AUG-2002 (first entry)
 XX Termamyl-like-alpha-amylase #2.
 DE Termamyl; alpha amylase; starch liquefaction; ethanol production;
 XX textile desizing; detergent; enzyme.
 KW Bacillus sp.
 OS WO200210355-A2.
 XX 07-FEB-2002.
 XX 12-JUL-2001; 2001WO-DK000488.
 XX 01-AUG-2000; 2000DK-00001160.
 XX 12-SEP-2000; 2000DK-00001354.
 XX 10-NOV-2000; 2000DK-00001687.
 XX 26-APR-2001; 2001DK-00000655.
 XX (NOVO) NOVOZYMES AS.
 XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 XX WPI; 2002-280633/32.
 XX N-PSDB; ABL96208.
 XX Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX Claim 8; Fig 1; 90pp; English.
 XX This invention relates to variants of a parent Termamyl-like alpha-

CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120plusOC and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60
 Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60
 Qy 61 YDLDLGEFNQKGTVRTKYGTRSQLESAIHALKNGVQVYGVVNMHKGADATENVLAV 120
 Db 61 YDLDLGEFNQKGTVRTKYGTRSQLESAIHALKNGVQVYGVVNMHKGADATENVLAV 120
 Qy 121 EVNPNRNRQELSGDYTTIEAWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFQNRKYKF 180
 Db 121 EVNPNRNRQELSGDYTTIEAWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFQNRKYKF 180
 Qy 181 RGDGKAMDWEVDSSENGYDYLMAVDVMDHDPVNVNLRWGEWYTTNTLNLDFRIDAVKH 240
 Db 181 RGDGKAMDWEVDSSENGYDYLMAVDVMDHDPVNVNLRWGEWYTTNTLNLDFRIDAVKH 240
 Qy 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWHSVDFVPLHYNLYNA 300
 Db 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWHSVDFVPLHYNLYNA 300
 Qy 301 SNSGNYDMAKLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 Db 301 SNSGNYDMAKLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 Qy 361 QGYPSVFYGDYIGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWREGNTT 420
 Db 361 QGYPSVFYGDYIGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWREGNTT 420
 Qy 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGTVTINADGWANFSVNGGSVS 480
 Db 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGTVTINADGWANFSVNGGSVS 480
 Qy 481 IWKVR 485
 Db 481 IWKVR 485

RESULT 13
 ABB99481
 ID ABB99481 standard; protein; 485 AA.
 XX AC ABB99481;
 XX DT 12-FEB-2003 (first entry)
 XX DE Amino acid sequence of an alpha-amylase.
 XX KW Alpha-amylase; enzyme; detergent; boric acid.
 XX OS Alkaliphilicbaciillus.
 XX PN WO200268575-A1.
 XX PD 06-SEP-2002.
 XX PF 25-FEB-2002; 2002WO-US005512.
 XX PR 28-FEB-2001; 2001US-00795211.
 XX PA (PROC) PROCTER & GAMBLE CO.
 XX

PI Kaesturi C, Wandrat MB, Song BX;
 XX WPI; 2003-058303/05.
 XX Aqueous liquid or gel type detergent, useful as automatic dishwashing
 PT composition, comprises boric acid or born compound, polyhydroxy compound,
 FT calcium ions and alpha-amylase enzyme.,
 XX
 PS Claim 1; Page 26-29; 36pp; English.
 XX The present sequence represents an alpha-amylase. The enzyme is used in
 CC detergents of the invention. The specification describes an aqueous
 CC liquid or gel type detergent composition, which comprises boric acid or a
 CC boron compound capable of forming boric acid in the composition, a
 CC polyhydroxy compound, calcium ions and selected alpha-amylase enzyme. The
 CC detergent composition is useful for stabilizing an amylase enzyme in an
 CC aqueous liquid or gel type detergent composition. It is useful for
 CC cleaning tableware (e.g. glassware, china, silverware, plastics),
 CC kitchenware, household surface such as floors, bathroom fixtures and
 CC countertops, and fabrics. It is useful as a fully formulated cleaning
 CC powder or as an additive or speciality product that is used alone or with
 CC other cleaning products. It is particularly useful in automatic
 CC dishwashing machine
 XX SQ Sequence 485 AA;

Query Match 100.0%; Score 2720; DB 6; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.2e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60
 Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSDVGYGA 60
 Qy 61 YDLDLGEFNQKGTVRTKYGTRSQLESAIHALKNGVQVYGVVNMHKGADATENVLAV 120
 Db 61 YDLDLGEFNQKGTVRTKYGTRSQLESAIHALKNGVQVYGVVNMHKGADATENVLAV 120
 Qy 121 EVNPNRNRQELSGDYTTIEAWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFQNRKYKF 180
 Db 121 EVNPNRNRQELSGDYTTIEAWTKFDPGKRGNTYSDFKRWYHFDGVDQSRQFQNRKYKF 180
 Qy 181 RGDGKAMDWEVDSSENGYDYLMAVDVMDHDPVNVNLRWGEWYTTNTLNLDFRIDAVKH 240
 Db 181 RGDGKAMDWEVDSSENGYDYLMAVDVMDHDPVNVNLRWGEWYTTNTLNLDFRIDAVKH 240
 Qy 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWHSVDFVPLHYNLYNA 300
 Db 241 IKYSFTDRDLTHVRNATGKEMFAVAEFWKNLDGALENYLNKTNWHSVDFVPLHYNLYNA 300
 Qy 301 SNSGNYDMAKLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 Db 301 SNSGNYDMAKLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
 Qy 361 QGYPSVFYGDYIGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWREGNTT 420
 Db 361 QGYPSVFYGDYIGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNNIIGWREGNTT 420
 Qy 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGTVTINADGWANFSVNGGSVS 480
 Db 421 HPNSGLATIMSDGPGGKEMVYGVQNKAGQVWHIDITGNKPGTVTINADGWANFSVNGGSVS 480
 Qy 481 IWKVR 485
 Db 481 IWKVR 485

RESULT 14
 AAB30701
 ID AAB30701 standard; protein; 834 AA.
 XX AC AAB30701;
 XX

DT 02-APR-2001 (first entry)
 XX A Bacillus pectate lyase and JP170 alpha-amylase fusion protein.
 XX
 XX Pectate lyase; pectinase; alpha-1,4-glycosidic linkage; pectic acid;
 XX polygalacturonic acid; alpha-amylase.
 XX
 XX Synthetic.
 OS Bacillus licheniformis.
 OS Escherichia coli.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..29
 FT /note= "signal peptide"
 FT Protein 30..343
 FT /note= "pectate lyase"
 FT Peptide 346..349
 FT /note= "IEGR linker"
 FT Protein 350..834
 FT /note= "alpha-amylase"
 XX
 XX WO200075344-A1.
 XX
 XX 14-DEC-2000.
 XX
 XX 31-MAY-2000; 2000WO-DK000296.
 XX
 XX 02-JUN-1999; 99DK-00000780.
 PR 11-JUN-1999; 99US-0138692P.
 XX
 XX (NOVO) NOVO NORDISK AS.
 PA
 XX Rasmussen MD, Bjoernvad ME, Diers I;
 PI WPI; 2001-071079/08.
 DR N-PSDB; AAC86598.
 XX
 XX Bacillus cells having a DNA sequence coding for a pectate lyase, a
 PT proteolytic cleavage target site, or a polypeptide of exogenous origin
 PT fused sequentially into one open reading frame, for producing fusion
 PT proteins in higher yields.
 XX
 XX Claim 18; Page 69-73; 94pp; English.
 PS
 XX The present sequence represents a fusion protein of a Bacillus pectate
 CC lyase polypeptide and a JP170 alpha-amylase polypeptide. Pectate lyase is
 CC a pectinase which catalyses the random cleavage of alpha-1,4-glycosidic
 CC linkages in pectic acid (polygalacturonic acid). The fusion polypeptide
 CC is expressed using the cells of the invention. The specification
 CC describes a cell for improved production of a fusion protein comprising a
 CC native pectate lyase fused to an exogenous polypeptide. The cell is
 CC preferably a gram positive cell. The cell is useful for the production of
 CC higher yields of fusion proteins or polypeptides, which have been
 CC difficult to obtain, such as active human antibodies
 XX
 XX Sequence 834 AA;
 SQ
 Query Match 100.0%; Score 2720; DB 4; Length 834;
 Best Local Similarity 100.0%; Pred. No. 6.9e-212;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HNGTGTGTMQYFEWHLPNDSNHLRDDASNLNRGITAIPPAWKGTSDNDVGYGA 60
 DB 350 HNGTGTGTMQYFEWHLPNDSNHLRDDASNLNRGITAIPPAWKGTSDNDVGYGA 409
 QY 61 YDLYDLGEFNQKQVTRTKYTRQLESALHALKXNGVQVYGVDMHKGADATENVLAV 120
 DB 410 YDLYDLGEFNQKQVTRTKYTRQLESALHALKXNGVQVYGVDMHKGADATENVLAV 469
 QY 121 EVNPNRNRNQBISGDYITIAWTKDFPGRGNVYDSEKRWYHFDGVWDQSDRQFNRIYKF 180
 DB 470 EVNPNRNRNQBISGDYITIAWTKDFPGRGNVYDSEKRWYHFDGVWDQSDRQFNRIYKF 529

QY 181 RGDGKAWDWEVDSENGNYDYLMTYADVMDHPEVNNELRRGWGYTNTLNDGFRIDAVKH 240
 DB 530 RGDGKAWDWEVDSENGNYDYLMTYADVMDHPEVNNELRRGWGYTNTLNDGFRIDAVKH 589
 QY 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENYLNKTNMHSVFDVPLHYNLYNA 300
 DB 590 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENYLNKTNMHSVFDVPLHYNLYNA 649
 QY 301 SNSGGNYDMAKLNGTVVQKHPMAHTVFDNDHDSQGESLESFVQEWFKPLAYALLITRE 360
 DB 650 SNSGGNYDMAKLNGTVVQKHPMAHTVFDNDHDSQGESLESFVQEWFKPLAYALLITRE 709
 QY 361 QGYPSVFYGDYIGIPTHSVPAKAKIDPILARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
 DB 710 QGYPSVFYGDYIGIPTHSVPAKAKIDPILARQNFAYGTQHDYFDHNNIIGWTREGNTT 769
 QY 421 HPNSGLATIMSDGPGGKEMVYQNKAGQVWHDDITGNKPGTVTINADGANFVNGGSVS 480
 DB 770 HPNSGLATIMSDGPGGKEMVYQNKAGQVWHDDITGNKPGTVTINADGANFVNGGSVS 829
 QY 481 IWKVR 485
 DB 830 IWKVR 834
 RESULT 15
 AAY07392
 ID AAY07392 standard; protein; 485 AA.
 XX
 AC AAY07392;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Wild type Termamyl(RTM)-like alpha-amylase protein #8.
 XX
 XX Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
 KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
 KW ethanol.
 XX
 OS Bacillus sp.
 XX
 XX WO9919467-A1.
 PN
 XX
 PD 22-APR-1999.
 XX
 PF 13-OCT-1998; 98WO-DK000444.
 XX
 PR 13-OCT-1997; 97DK-00001172.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Svendsen A, Borchert TV, Bisgard-Frantzen H;
 XX
 DR WPI; 1999-277632/23.
 XX
 PT Variant alpha-amylases - useful as detergents or for textile desizing or
 PT starch liquefaction.
 XX
 PS Disclosure; Page 74-76; 93pp; English.
 XX
 CC This sequence represents the parent sequence for new variants of a parent
 CC Termamyl-like alpha-amylase with alpha-amylase activity. The variants
 CC comprise mutations in 2-6 regions/positions relative to an alpha-amylase
 CC from either of two Bacillus species in WO9526397, B. stearothermophilus,
 CC B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
 CC amylase variants are detergent additives for use in detergents for
 CC dishwashing, manual or automatic laundry. The variants can also be used
 CC for textile desizing or starch liquefaction (e.g. for production of
 CC sweeteners or ethanol)
 XX
 SQ Sequence 485 AA;

Query Match

99.7%; Score 2712; DB 2; Length 485;

Best Local Similarity 99.8%; Pred. No. 1.4e-211;		Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	HHNGTNGTMMQYFEWHLFNDGNHWNRLRDDASNLNRNGITAIWI	PPPAWKGTSONDVG YGA 60
Db	1	HHNGTNGTMMQYFEWHLFNDGNHWNRLRDDASNLNRNGITAIWI	PPPAWKGTSONDVG YGA 60
Qy	61	YDLYDLGEFQKQKGTVRTKYGTRSQLESIAIHALKXNGVQVYGD	VVMNHKGGADATENVLAV 120
Db	61	YDLYDLGEFQKQKGTVRTKYGTRSQLESIAIHALKXNGVQVYGD	VVMNHKGGADATENVLAV 120
Qy	121	EVNPNNEQETSGDYTTIEATWKPDPPGRGNTYSDFKRWYHFDG	VDWDQSRQFQNR IYKF 180
Db	121	EVNPNNEQETSGDYTTIEATWKPDPPGRGNTYSDFKRWYHFDG	VDWDQSRQFQNR IYKF 180
Qy	181	RGDGKAWDWEVDSSENGNYDILMYADVMDHPEVVNELRRWGE	WYTTNTLNLDGFRIDAVKH 240
Db	181	RGDGKAWDWEVDSSENGNYDILMYADVMDHPEVVNELRRWGE	WYTTNTLNLDGFRIDAVKH 240
Qy	241	IKYSFTRDMLTHVRNATGKMFVAEAFWKNDLGALENYLNKTN	NHSHVDFVPLHYNLYNA 300
Db	241	IKYSFTRDMLTHVRNATGKMFVAEAFWKNDLGALENYLNKTN	NHSHVDFVPLHYNLYNA 300
Qy	301	SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLES	FVOEWFKPLAYALILTRE 360
Db	301	SNSGGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLES	FVOEWFKPLAYALILTRE 360
Qy	361	QGYPSVFYGYGIPTHSVPAKAKIDPILFARONFAYGTOHDY	FDDHNIIGWTREGNTT 420
Db	361	QGYPSVFYGYGIPTHSVPAKAKIDPILFARONFAYGTOHDY	FDDHNIIGWTREGNTT 420
Qy	421	HPNSGLATIMSDGPGGKMWYVGQNKAGQVWHDDITGNKPGT	VTITINADGWANFSVNGGSVS 480
Db	421	HPNSGLATIMSDGPGGKMWYVGQNKAGQVWHDDITGNKPGT	VTITINADGWANFSVNGGSVS 480
Qy	481	IWKR	485
Db	481	IWKR	485

Search completed: October 7, 2004, 00:12:13
Job time : 60.5516 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-4
Perfect score: 2720
Sequence: 1 HHNGTNGTMMQYFEWHLNDP.....ADGWANFVNGSGSVSIWKR 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2440	89.7	516	2	082839
2	1984	72.9	533	2	09AQ54
3	1976	72.6	513	16	081A54
4	1967	72.3	513	16	081VJ4
5	1910.5	70.2	613	2	059222
6	1903	70.0	519	2	03RQ78
7	1899.5	69.5	549	2	031193
8	1894.5	69.3	521	2	071034
9	1894.5	69.3	549	2	09KW76
10	1860.5	68.4	501	2	031I48
11	1556.5	57.2	507	16	087HG6
12	1374	50.5	481	16	089IF1
13	1373	50.5	493	2	030367
14	1296.5	47.7	486	16	08DT08
15	1279.5	47.0	488	16	08EOM2
16	1276.5	46.9	488	16	08E696

17	1267	46.6	484	16	Q97Q49	Q97Q49 streptococc
18	1265	46.5	484	16	Q8DPC8	Q8DPC8 streptococc
19	1257.5	46.2	486	2	O68875	O68875 streptococc
20	1245	45.8	492	16	Q8YU21	Q8YU21 anabaena sp
21	1238.5	45.5	485	2	Q53786	Q53786 streptococc
22	1235.5	45.4	484	2	O50583	O50583 streptococc
23	1143	42.0	491	16	Q9CG59	Q9CG59 lactococcu
24	1104	40.6	506	16	Q8U916	Q8U916 agrobacteri
25	1072	39.4	494	16	Q8Z5S5	Q8Z5S5 salmonella
26	1071	39.4	495	16	Q8XBB6	Q8XBB6 escherichia
27	1069	39.3	495	16	Q8FGL8	Q8FGL8 escherichia
28	1062	39.0	495	16	Q7UAB0	Q7UAB0 shigella fl
29	1060	39.0	495	16	Q83R40	Q83R40 shigella fl
30	1027.5	37.8	529	3	Q877B1	Q877B1 aspergillus
31	507.5	18.7	461	1	O33476	O33476 pyrococcus
32	506	18.6	461	1	Q8NKR4	Q8NKR4 thermococcu
33	492	18.1	460	1	Q9P9L0	Q9P9L0 pyrococcus
34	492	18.1	460	1	O08452	O08452 pyrococcus
35	492	18.1	473	17	Q8U3I9	Q8U3I9 pyrococcus
36	490	18.0	461	1	Q8NKR5	Q8NKR5 thermococcu
37	485	17.8	469	1	O50200	O50200 thermococcu
38	480	17.6	432	14	Q8JZK3	Q8JZK3 uncultured
39	467	17.2	457	1	Q93647	Q93647 thermococcu
40	322.5	11.9	482	2	Q60051	Q60051 thermoactin
41	298.5	11.0	421	10	Q7X9T1	Q7X9T1 phaseolus a
42	296	10.9	420	10	Q9ZP43	Q9ZP43 phaseolus v
43	293	10.8	424	10	Q8LP27	Q8LP27 pharbitis n
44	288	10.6	423	10	Q42678	Q42678 cuscata ref
45	285	10.5	416	10	Q8LJQ6	Q8LJQ6 musa acumin

ALIGNMENTS

RESULT 1

ID	082839	PRELIMINARY;	PRT;	516 AA.
AC	082839;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Amylase.			
OS	Bacillus sp.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1409;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=KSM-1378;			
RX	MEDLINE=98342096; PubMed=9675143;			
RA	Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,			
RA	Ozaki K., Ito S.;			
RT	"Improved thermostability of a Bacillus alpha-amylase by deletion of			
RT	an arginine-glycine residue is caused by enhanced calcium binding."			
RL	Biochem. Biophys. Res. Commun. 248:372-377(1998).			
DR	EMBL; AB008763; BAA32431.1; -.			
DR	HSSP; P06278; 1VJS.			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha amyl cat.			
DR	InterPro; IPR006589; Alp_ami1_cat sub.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAAMYLASE.			
DR	SMART; SMO0642; Amy; 1.			
SQ	SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;			

Query Match 89.7%; Score 2440; DB 2; Length 516;

Best Local Similarity 86.6%; Pred. No. 6.3e-148; Mismatches 25; Indels 0; Gaps 0;

Matches 420; Conservative 40; Yy 1 HHNGTNGTMMQYFEWHLNDPNDGNHNRRLDDASNLNRNGITAIWTPPAWKGTQNDVGYGA 60
Db 32 HHNGTNGTMMQYFEWHLNDPNDGNHNRRLDDAANLKSIGITAVWTPPAWKGTQNDVGYGA 91

```
QY 61 YDYLDFEFNKGKGTVRTKYKTRTSOLESIAIHALKNNGVQVYGVVMMHKGADATENVLAV 120
DB 92 YDYLDFEFNKGKGTVRTKYKTRSQLOQAVTSLKXNGLOVYGVVMMHKGADGTWNAV 151
QY 121 EVNPNRNQISGYDTTIEAWTKDFPGRGNTYSDFKRWYTHFDGVMDQSRQFQNRRIYKF 180
DB 152 EVNRSNRNQBISGEYTTIEAWTKDFPGRGNTSHSNFKRWYTHFDGTDWDQSRQLQNKIYKF 211
QY 181 RGPCKAWDEVDSENGNYDYLMAVDMDHPEVNVNELRRGEWVNTNLNDGFRIDAVKH 240
DB 212 RGTGKAWDEVDSENGNYDYLMAVDMDHPEVNVNELRRGEWVNTNLNDGFRIDAVKH 271
QY 241 IKYSFTFRLWLTHTVRNATGKEMFAVAEFWKNDLGALENLYNKTNNHNSVDFVPLHYNLNA 300
DB 272 IKYSFTFRLWLTHTVRNATGKEMFAVAEFWKNDLGALENLYNKTNNHNSVDFVPLHYNLNA 331
QY 301 SNSSGNYDMAKLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
DB 332 SNSSGYPDMRNLNGSVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 391
QY 361 QGYPSPYFGYDYGIPHTSVPMKAKIDPILBARQNFAYGTHQDHYFDHNNIIGTWREGNTT 420
DB 392 QGYPSPYFGYDYGIPHTSVPMKAKIDPILBARQNFAYGTHQDHYFDHNNIIGTWREGDSS 451
QY 421 HPNSGLATIMSDGPGGKMMYVGNKAGOVVHDIITGNKPGCTVTINADGWANFVNGGSVS 480
DB 452 HPNSGLATIMSDGPGGKMMYVGNKAGOVVHDIITGNKPGCTVTINADGWANFVNGGSVS 511
QY 481 IWVKR 485
DB 512 VVVKQ 516

RESULT 2
Q9AQ54
ID Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
RT KSM B-404."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 72.9%; Score 1984; DB 2; Length 533;
Best Local Similarity 71.2%; Pred. No. 9.1e-119;
Matches 344; Conservative 58; Mismatches 77; Indels 4; Gaps 2;

QY 6 NGTMMQYFEWHLNDGNHNRDRDASNLNRNGITAIWIIPPAWKGTSONDVGAYDLYD 65
DB 52 NGTMMQYFEWHLNDGNHNRDRDASNLNRNGITAIWIIPPAWKGTSONDVGAYDLYD 111
QY 66 LGFEFNKGKGTVRTKYKTRTSOLESIAIHALKNNGVQVYGVVMMHKGADATENVLAVNPN 125
DB 112 LGFEFNKGKGTVRTKYKTRTSOLESIAIHALKNNGVQVYGVVMMHKGADATENVLAVNPN 171
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QY 126 NRNOEISGDTTIEAWTKDFPGRGNTYSDFKRWYTHFDGVMDQSRQFQNRRIYKFRGDGK 185
DB 172 NRNVESGDEYISAWTKDFPGRGNTYSDFKRWYTHFDGVMDQSRQFQNRRIYKFRGIGK 230
QY 186 AMDWEVDSNGNYDYLMAVDMDHPEVNVNELRRGEWVNTNLNDGFRIDAVKHIIKYSF 245
DB 231 AMDWEVSSNGNYDYLMAVDMDHPEVNVNELRRGEWVNTNLNDGFRIDAVKHIDHEY 290
QY 246 TRDMLTHVRNATGKEMFAVAEFWKNDLGALENLYNKTNNHNSVDFVPLHYNLNANSNG 305
DB 291 LRDMVNVHVRQQTGKEMFAVAEFWKNDLGALENLYNKTNNHNSVDFVPLHYNFHYASKNG 350
QY 306 NYDMAKLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTREGQYPS 365
DB 351 NYDMRNILAGTVVANHPTLAVTLVENHDSQPQGESLESFVQEWFKPLAYALILTREGQYPS 410
QY 366 VFVGDYIGTPTHS---VPAMKAKIDPILBARQNFAYGTHQDHYFDHNNIIGTWREGNTTTP 422
DB 411 VFVGDYIGTPTHS---VPAMKAKIDPILBARQNFAYGTHQDHYFDHNNIIGTWREGDVSVA 470
QY 423 NSGLATIMSDGPGGKMMYVGNKAGOVVHDIITGNKPGCTVTINADGWANFVNGGSVSIIW 482
DB 471 NSGLATIMSDGPGGKMMYVGNKAGOVVHDIITGNKPGCTVTINADGWANFVNGGSVSIIY 530
QY 483 VKR 485
DB 531 VQR 533

RESULT 3
Q81AS4
ID Q81AS4 PRELIMINARY; PRT; 513 AA.
AC Q81AS4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Calleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AB017009; AAP10417.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Aamy; 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BFF9FF6 CRC64;

Query Match 72.6%; Score 1976; DB 16; Length 513;
Best Local Similarity 71.0%; Pred. No. 2.8e-118;
Matches 343; Conservative 57; Mismatches 79; Indels 4; Gaps 2;

QY 6 NGTMMQYFEWHLNDGNHNRDRDASNLNRNGITAIWIIPPAWKGTSONDVGAYDLYD 65
DB 32 NGTMMQYFEWHLNDGNHNRDRDASNLNRNGITAIWIIPPAWKGTSONDVGAYDLYD 91
QY 66 LGFEFNKGKGTVRTKYKTRTSOLESIAIHALKNNGVQVYGVVMMHKGADATENVLAVNPN 125
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Db 92 LGFENQSGTTRTKYGTGAQLKSAIDALHKKNDYDGVWNNHKGADYTETVTAVEVDPS 151
Qy 126 NRQOEISGDYITAEWTKFDPFGRGNTYSDFKRWYHFDGVDWDSQSFQNRIRYKFRGDGK 185
Db 152 NRNVESGDYIEISAWTGFNPFGRGDSYSNFKWKYHFDGTDWDSGRKL-NRIYKFRGIGK 210
Qy 186 AWDWEVDSENGNDYLMYADVMDHPVNNELRWGEWYTNLNLDFRIDAVIDKHIXSP 245
Db 211 AWDWEVSENGNDYLMYADLDLDPDPVANEMKNGWTYANELNLDFRIDAVIDKHIDHEY 270
Qy 246 TRDLWTHVRNATGKEMFAVAFWKNQDILGALENYLNKNNHNSVDPVPLHYNLYNASGG 305
Db 271 LRDNWVNRQGTGKEMFTVAEYQNDIOTLNNYLAKVNYNSQSFDAPLHYNFHYASTGNG 330
Qy 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGSGLESFVQWFKPLAYALILITREQGYPS 365
Db 331 NYDMRNLTGTVVANHPTLAFTLVNHDSPGSGLESFVSPWPKPLAYAFILITRAEGYPS 390
Qy 366 VFYGDYIGTIPHS---VPAMKAKIDPILAEARONFAYGTQHDYFDHNNIIGWTRGNTTHP 422
Db 391 VFYGDYIGTSGNSYEIPALKDKIDPILTARKNFAYGTQRDYFDHPDVGWTRGDSVHA 450
Qy 423 NSGLATIMSDPGGKMWYVQNKAGQVHMDITGNKFGTGTINADGWANFVSGSVSIW 482
Db 451 NSGLATLISDGPAGKMWVGNKNAVGVYDITGNQNTVTINKDQGWQFVSGSVSIY 510
Qy 483 VKR 485
Db 511 VQ 513

RESULT 4
Q81YJ4 PRELIMINARY; PRT; 513 AA.
ID Q81YJ4
AC Q81YJ4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapfle E.K., Ostad O.A., Helgason E., Rikstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Winn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR Pfam; PF00128; Alp amyl cat_sub.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 5586D6EF28FD159B CRC64;

Query Match 72.3%; Score 1967; DB 16; Length 513;
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Best Local Similarity 70.6%; Pred. No. 1.1e-117;
Matches 341; Conservative 57; Mismatches 81; Indels 4; Gaps 2;

Qy 6 NGTMQYFEWHLNDGNNHNRRLRDDASNLNRGITAIIWIPPAWKGTSQNDVGYGAYDIYD 65
Db 32 NGTLMQYFEWYAPSDRNHNRRLRTDAENLAQKGITSWIPPAWKGTTQNDVGYGAYDIYD 91
Qy 66 LGFENQSGTTRTKYGTGRSOLSAIHALKNNGVQYGVVNNHKGADATENVLAVENPN 125
Db 92 LGFENQSGTTRTKYGTGAQLKSAIEALHKKNDYDGVWNNHKGADYTETVTAVEVDN 151
Qy 126 NRQOEISGDYITAEWTKFDPFGRGNTYSDFKRWYHFDGVDWDSQSFQNRIRYKFRGDGK 185
Db 152 NRNVESGDYIEISAWTGFNPFGRGDSYSNFKWKYHFDGTDWDSGRKL-NRIYKFRGIGK 210
Qy 186 AWDWEVDSENGNDYLMYADVMDHPVNNELRWGEWYTNLNLDFRIDAVIDKHIXSP 245
Db 211 AWDWEVSENGNDYLMYADLDLDPDPVANEMKNGWTYANELNLDFRIDAVIDKHIDHEY 270
Qy 246 TRDLWTHVRNATGKEMFAVAFWKNQDILGALENYLNKNNHNSVDPVPLHYNLYNASGG 305
Db 271 LRDNWVNRQGTGKEMFTVAEYQNDIOTLNNYLAKVNYNSQSFDAPLHYNFHYASKNG 330
Qy 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGSGLESFVQWFKPLAYALILITREQGYPS 365
Db 331 NYDMRNLTGTVVQNHHPALAVTLVNHDSQPGSGLESFVSPWFKPLAYAFILITRAEGYPS 390
Qy 366 VFYGDYIGI---PTHSPVAMKAKIDPILAEARONFAYGTQHDYFDHNNIIGWTRGNTTHP 422
Db 391 VFYGDYIGTSGNSYEIPALKDKIDPILTARKNFAYGTQRDYFDHPDVGWTRGDSVHA 450
Qy 423 NSGLATIMSDPGGKMWYVQNKAGQVHMDITGNKFGTGTINADGWANFVSGSVSIW 482
Db 451 NSGLATLISDGPAGKMWVGNKNAVGVYDITGNQNTVTINKDQGWQFVSGSVSIY 510
Qy 483 VKR 485
Db 511 VQ 513

RESULT 5
Q59222 PRELIMINARY; PRT; 613 AA.
ID Q59222
AC Q59222;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.2.1).
GN AMY.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RA Lin L.-L., Chu W.S., Hsu W.H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22045; AAA63900.1; -.
DR HSPF; P06278; IVUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp amyl_cat_sub.
DR InterPro; IPR002044; CBD 4.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PRO0110; ALPHAMYLASE.
DR ProDom; PD001568; CBD 4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
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SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
Query Match 70.2%; Score 1910.5; DB 2; Length 613;
Best Local Similarity 69.2%; Pred. No. 5.4e-114;
Matches 332; Conservative 63; Mismatches 84; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLPLNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSDNDVGYGAYDLY 65
DB 36 NETMMQYFEWDLNDGTLTKVNEARLSSLGITALLPAPYKGTSDNDVGYGVYDLY 95

QY 66 LGFEFNQKGTVRTKGYTRSQLESIAHALKKNQGVQYGVVMMHKGADATENVLAVENP 125
DB 96 LGFEFNQKGTVRTKGYTRSQLESIAHALKKNQGVQYGVVMMHKGADATENVLAVENP 125

QY 125 NNRNQEISGDYTIKAWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKRGD 184
DB 156 NNRNQEISGDYTIKAWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKRGD 184

QY 185 KAWDWEVDSNGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 244
DB 214 KAWDWEVDSNGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 244

QY 245 ANDWEVDVTEGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 274
DB 274 ANDWEVDVTEGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 274

QY 246 TRDLWTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNMHSVDFVPLHYNLYNASNG 305
DB 334 TRDLWTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNMHSVDFVPLHYNLYNASNG 305

QY 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSDPGESLESFVQWFKPLAYALILTREGYPS 365
DB 394 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSDPGESLESFVQWFKPLAYALILTREGYPS 365

QY 366 VFGYDYGIPKYNIPGLKSKIDLLARRDYAGTQBDYIDHQDILGWTREGIDTFPNSG 454
DB 454 VFGYDYGIPKYNIPGLKSKIDLLARRDYAGTQBDYIDHQDILGWTREGIDTFPNSG 454

QY 426 LATIMSDGPGGKEMWYQKAGQVWHDITGNKPGTGTINADGWANFSVNGGVSIVWKR 485
DB 514 LATIMSDGPGGKEMWYQKAGQVWHDITGNKPGTGTINADGWANFSVNGGVSIVWKR 485

RESULT 6
Q9RQT8 PRELIMINARY; PRT; 519 AA.
AC Q9RQT8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF0567.1; --
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT CHAIN 58 519 RAW STARCH DIGESTING AMYLASE.
SQ SEQUENCE 519 AA; 58337 MW; 3E6B88A4DF98B163 CRC64;

Query Match 70.0%; Score 1903; DB 2; Length 519;
Best Local Similarity 67.8%; Pred. No. 1.3e-113;
Matches 328; Conservative 72; Mismatches 80; Indels 4; Gaps 2;

SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC2895E8 CRC64;
Query Match 70.2%; Score 1910.5; DB 2; Length 613;
Best Local Similarity 69.2%; Pred. No. 5.4e-114;
Matches 332; Conservative 63; Mismatches 84; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLPLNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSDNDVGYGAYDLY 65
DB 36 NETMMQYFEWDLNDGTLTKVNEARLSSLGITALLPAPYKGTSDNDVGYGVYDLY 95

QY 66 LGFEFNQKGTVRTKGYTRSQLESIAHALKKNQGVQYGVVMMHKGADATENVLAVENP 125
DB 96 LGFEFNQKGTVRTKGYTRSQLESIAHALKKNQGVQYGVVMMHKGADATENVLAVENP 125

QY 125 NNRNQEISGDYTIKAWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKRGD 184
DB 156 NNRNQEISGDYTIKAWTKFDPGRGNTYSDFKRWVYHFDGVDWDSRQFQNRILYKRGD 184

QY 185 KAWDWEVDSNGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 244
DB 214 KAWDWEVDSNGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 244

QY 245 ANDWEVDVTEGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 274
DB 274 ANDWEVDVTEGNDYLMYADVDMDHPEVNNELRRWGEWYTNLTNLGDFRIDAVKHIKYS 274

QY 246 TRDLWTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNMHSVDFVPLHYNLYNASNG 305
DB 334 TRDLWTHVRNATGKEMPAFAVAFKWNKDLGALENYLNKTNMHSVDFVPLHYNLYNASNG 305

QY 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSDPGESLESFVQWFKPLAYALILTREGYPS 365
DB 394 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSDPGESLESFVQWFKPLAYALILTREGYPS 365

QY 366 VFGYDYGIPKYNIPGLKSKIDLLARRDYAGTQBDYIDHQDILGWTREGIDTFPNSG 454
DB 454 VFGYDYGIPKYNIPGLKSKIDLLARRDYAGTQBDYIDHQDILGWTREGIDTFPNSG 454

QY 426 LATIMSDGPGGKEMWYQKAGQVWHDITGNKPGTGTINADGWANFSVNGGVSIVWKR 485
DB 514 LATIMSDGPGGKEMWYQKAGQVWHDITGNKPGTGTINADGWANFSVNGGVSIVWKR 485

RESULT 7
O31193 PRELIMINARY; PRT; 549 AA.
AC O31193
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha amylase.
GN AMI.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF032864; AAB86961.1; --
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

Query Match 69.5%; Score 1889.5; DB 2; Length 549;
Best Local Similarity 67.7%; Pred. No. 1e-112;
Matches 325; Conservative 73; Mismatches 81; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLPLNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSDNDVGYGAYDLY 65
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Db 39 NGTMMQYFEWYLPDDGLTWKTVKVAEANNLSLGTALWLPAYKGTSDVGYGYDLYD 98
Qy 66 LGFBNQKGTVRTKYTGTRTSQLESALHALKNNGVQYGVDMVNNHKGADATENLVAVEVNP 125
Db 99 LGFBNQKGTVRTKYTGTRTSQLESALHALKNNGVQYGVDMVNNHKGADATENLVAVEVNP 158
Qy 126 NRQNEISGDTYIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDSQROFQNRKYKFRGDK 185
Db 159 DRNQEISGTYQIAWTKFDPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 AWDWEVDSNGNDYLMYADVMDHPVNNELRWGEWYTNLTNLDGFRIDAVKHKYSF 245
Db 218 AWDWEVDTEGNDYLMYADVMDHPVNNELRWGEWYTNLTNLDGFRIDAVKHKYSF 277
Qy 246 TRDWLTHVRNATGKEMPAFAEFKNDLGCALENYLNKTNWHSVDFVPLHYNLYNASGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNFYTASKSG 337
Qy 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLSEFVQWFKPLAYALILTREQGYPS 365
Db 338 AFDWRTLTMTLMDQPTLAVTFVDNHDTEPGQALQSWVDWFKPLAYAFILTRQEGYPC 397
Qy 366 VFYGDYGIPTSHVPAMKAKIDPILKARONFAYGTOHDYFDHNNIIGWTRGNTTHPNSG 425
Db 398 VFYGDYGIPTSHVPAMKAKIDPILKARONFAYGTOHDYFDHNNIIGWTRGNTTHPNSG 457
Qy 426 LATIMSDPGGKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVNGSGSVIWK 485
Db 458 LAALITDPPGSKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVNGSGSVIWK 517
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RESULT 8

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P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
RL thermotable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; BAB18785.1; -.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami cat.
DR InterPro; IPR006589; Alp_ami cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL 1 34 POTENTIAL.
FT CHAIN 35 521 ALPHA-AMYLASE.
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;
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Query Match 69.3%; Score 1884.5; DB 2; Length 521;
Best Local Similarity 67.5%; Pred. No. 2e-112;
Matches 324; Conservative 73; Mismatches 82; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPDDGLTWKTVKVAEANNLSLGTALWLPAYKGTSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGLTWKTVKVAEANNLSLGTALWLPAYKGTSDVGYGYDLYD 98
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Qy 66 LGFBNQKGTVRTKYTGTRTSQLESALHALKNNGVQYGVDMVNNHKGADATENLVAVEVNP 125
Db 99 LGFBNQKGTVRTKYTGTRTSQLESALHALKNNGVQYGVDMVNNHKGADATENLVAVEVNP 158
Qy 126 NRQNEISGDTYIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDSQROFQNRKYKFRGDK 185
Db 159 DRNQEISGTYQIAWTKFDPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 AWDWEVDSNGNDYLMYADVMDHPVNNELRWGEWYTNLTNLDGFRIDAVKHKYSF 245
Db 218 AWDWEVDTEGNDYLMYADVMDHPVNNELRWGEWYTNLTNLDGFRIDAVKHKYSF 277
Qy 246 TRDWLTHVRNATGKEMPAFAEFKNDLGCALENYLNKTNWHSVDFVPLHYNLYNASGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNFYTASKSG 337
Qy 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLSEFVQWFKPLAYALILTREQGYPS 365
Db 338 AFDWRTLTMTLMDQPTLAVTFVDNHDTEPGQALQSWVDWFKPLAYAFILTRQEGYPC 397
Qy 366 VFYGDYGIPTSHVPAMKAKIDPILKARONFAYGTOHDYFDHNNIIGWTRGNTTHPNSG 425
Db 398 VFYGDYGIPTSHVPAMKAKIDPILKARONFAYGTOHDYFDHNNIIGWTRGNTTHPNSG 457
Qy 426 LATIMSDPGGKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVNGSGSVIWK 485
Db 458 LAALITDPPGSKMWYGVQKAGQVHDDITGNKPGTGTINADGWANFVNGSGSVIWK 517

RESULT 9
Q9KWY6
ID Q9KWY6 PRELIMINARY; PRT; 549 AA.
AC 09KWY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_ami cat.
DR InterPro; IPR006589; Alp_ami cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3B66DF91208CE CRC64;

Query Match 69.3%; Score 1884.5; DB 2; Length 549;
Best Local Similarity 67.5%; Pred. No. 2.2e-112;
Matches 324; Conservative 73; Mismatches 82; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPDDGLTWKTVKVAEANNLSLGTALWLPAYKGTSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGLTWKTVKVAEANNLSLGTALWLPAYKGTSDVGYGYDLYD 98

Qy 66 LGFBNQKGTVRTKYTGTRTSQLESALHALKNNGVQYGVDMVNNHKGADATENLVAVEVNP 125
Db 99 LGFBNQKGTVRTKYTGTRTSQLESALHALKNNGVQYGVDMVNNHKGADATENLVAVEVNP 158
Qy 126 NRQNEISGDTYIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDSQROFQNRKYKFRGDK 185
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Db 322 SGGYDRQRMNGTLMKONPVKATLVNHDHTQLOALESTVDWFWFKPLAYAFILLREEG 381
Qy 363 YPSVFYGDYTG-----IPTHSVPMKAKIDPILAEARONFAYGTQHDYFDHNNIIGW 413
Db 382 YPSVFYADYGAQYSDRGYNINAKVP-----YIEELVTLRKEYAYGKNSYLDHWDVIGW 437
Qy 414 TRENTTHPSGLATIMSDGPGKWMYVQNKAGQVWHDITGNKPGTIVTINADGNANFS 473
Db 438 TREGDABHPS--MAVIMSDGPGGTWMTYKPSRYV--DKLGIRTBVMTDANGMAEFP 494
Qy 474 VNGGSVSTW 483
Db 495 VNGGSVSVW 504

RESULT 12
ID Q89YP1 PRELIMINARY; PRT; 481 AA.
AC Q89YP1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN Bt4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 50.5%; Score 1374; DB 16; Length 481;
Best Local Similarity 50.2%; Pred. No. 7.6e-80;
Matches 241; Conservative 91; Mismatches 146; Indels 2; Gaps 2;

Qy 6 NGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIWIPPAWKTSDNDVGYGAYDLYD 65
Db 3 NGVMQYFEWHLPNNGDKLWKOIKEDALHLDIGYTAWIPPAWKADEQQDEGYATDLYD 62
Qy 66 LGFENQGTVRTKYGTQSLSAHLKNNQGVQYGVDMVNMHKGADATENVLAVENPN 125
Db 63 LGFEDQGTIRTKYTKDELKMDLHLYHIAVLVDVNLHKGAGDTEFKFVVEVDPK 122
Qy 126 NRNQEISGDYTIETAWTKFDFPGRNTYSDPKRWYHFDGVDWDSQRFQNRIFYKRGDGK 185
Db 123 ERTKALGEPFELQGTWGSFGRKDKSDFKWHWYHFGTGFDDA-QKRSQVFIQBGK 181
Qy 186 AWDMEVSENGNYDLYMADVMDHPPEVNLNRGEWYTNLNDGFRIDAVKHICYSP 245
Db 182 AWSGVDSENGNYDPLLCNDLDLHPPEVSENLNRGWKWSNELNDGMRDLAKHMKDQF 241
Qy 246 TRDWLTHVRNATKEMFAVAFWKNDLGALENLKNWNHNSVDPVPLHLYNLSNMSG 305
Db 242 VAQELDAVRBERGNDFYAVGSYWGNDLEALDAYEAVGHKNLFDVPLHYNFQASQEGK 301
Qy 306 NYDMAKLINGTVQKHPHVAFTFVDNHDSPQGESLESFVQBFKPLAYALILTREQGYS 365

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Db 302 DYDLRDLKDTLVEHHPDLAVTIVDNDHTORGSLNESNVEDWFKPLAYGLILLMKEGPC 361
Qy 366 VFYGDYGYGIPTHSVPMKAKIDPILAEARONFAYGTQHDYFDHNNIIGWREGTTHPSNG 425
Db 362 LFYGDYGYGKGEKSPHTRI-IDILLDARRKAYAGDQIEYFDHPSTIGFIRTGDEHNSG 420
Qy 426 LATIMSDGPGKWMYVQNKAGQVWHDITGNKPGTIVTINADGNANFSVNSIWK 485
Db 421 LVFLMSNDEAGSKIMSGLGKHGEVWHEITGSIIEITLDEEGNGEFSFERNLAVWVK 480

RESULT 13
ID Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSP; P06278; IVS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;

Query Match 50.5%; Score 1373; DB 2; Length 493;
Best Local Similarity 51.3%; Pred. No. 9.1e-80;
Matches 245; Conservative 81; Mismatches 150; Indels 2; Gaps 2;

Qy 6 NGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIWIPPAWKTSDNDVGYGAYDLYD 65
Db 4 NHTMMQFEWHLAADGHWKRLAEMAPELKAGIDTVVPPVTKAVSAETGYGVYDLYD 63
Qy 66 LGFENQGTVRTKYGTQSLSAHLKNNQGVQYGVDMVNMHKGADATENVLAVENPN 125
Db 64 LGFEDQGTVRTKYGTQELIEALAEQCKNGIAVYVLDVNMHKGADETEVEFKVIEVDPN 123
Qy 126 NRNQEISGDYTIETAWTKFDFPGRNTYSDPKRWYHFDGVDWDSQRFQNRIFYKRGDGK 185
Db 124 DRTKEISPEFIEGTWTKFTFPGDQYSSPKWNSHFNGTDFD-AREERTGVFRAGENK 182
Qy 186 AWDMEVSENGNYDLYMADVMDHPPEVNLNRGEWYTNLNDGFRIDAVKHICYSP 245
Db 183 KNWENDDFNGYDNPANIDYVNHDPVRRMDWGMKWLIDTLQCGFRDLAKIHNEF 242
Qy 246 TRDWLTHVRNATKEMFAVAFWKNDLGALENLKNWNHNSVDPVPLHLYNLSNMSG 305
Db 243 IKEFAAEWIRKQGFYIVGFEFWSNLDA CREFLDTVDYQIDLFVSLHYKLHEASLKR 302
Qy 306 NYDMAKLINGTVQKHPHVAFTFVDNHDSPQGESLESFVQBFKPLAYALILTREQGYS 365
Db 303 DFDSLKIFDDTLVQTHPTAVTFVDNHDSPHEALESWIGDWFKPSAYALTLLRRDGYVP 362
Qy 366 VFYGDYGYI-PTHSVPMKAKIDPILAEARONFAYGTQHDYFDHNNIIGWREGTTHPS 424
Db 363 VFYGDYGYIGPEPVDGKKELIDLLSARCNKAYGEQEDYFDHANTIGWVRGVEETEGS 422
Qy 425 GLATIMSDGPGKWMYVQNKAGQVWHDITGNKPGTIVTINADGNANFSVNSIWK 482

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301	QNRDFDMRTTFDDSLVDINPEYAVTFVENHDTQSGALESVEDWFKPLAYGLILLRQQG	360
Db	...	
363	YPSVFYGDYVIP-THSVPAWKADIPLEARQNFAYGTOHDYFDHNNIIIGWTREGNTH	421
Qy	...	
361	TPCLFYGDYVIGQGEFGQSFKEVIDKMAELRQNYVFGKVDYFTHSNCIGWTCILGDBEH	420
Db	...	
422	PNSGLATIMSDGPGGEKWMYVQNKAGQVWHDIITGNKPGTVTINADGWANFSVNGGSVSI	481
Qy	...	
421	-NSCLAVVLNTNGDQGWKHEVGEIYAGKTFVDYLGNCBQEVYVIGDDGWDGLVESASISA	479
Db	...	
482	WVKR	485
Qy	...	
480	WVPK	483
Db	...	

Search completed: October 7, 2004, 00:18:55
Job time : 47.501 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-4
Perfect score: 2720
Sequence: 1 HHNGTGTMMQYFEWHLPN.....ADGMANFVNGSGSVIWKVR 485
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2414	88.8	518	1 A27705	alpha-amylase (EC
2	1947	71.6	512	1 ALBSL	alpha-amylase (EC
3	1888.5	69.4	549	1 A24549	alpha-amylase (EC
4	1887.5	69.4	549	1 A54541	alpha-amylase (EC
5	1880.5	69.1	549	1 A24436	alpha-amylase (EC
6	1871	68.8	514	1 ALBSN	alpha-amylase (EC
7	1816	66.8	548	1 ALBSF	alpha-amylase (EC
8	1373	50.5	493	2 S15713	alpha-amylase (EC
9	1267	46.6	484	2 G95160	alpha-amylase (imp
10	1265	46.5	484	2 F98026	alpha-amylase (EC
11	1245	45.8	492	2 AH2079	alpha-amylase (imp
12	1143	42.0	491	2 C86781	alpha-amylase (imp
13	1104	40.6	506	2 G98247	cytoplasmic alpha-
14	1103	40.6	495	2 AD3038	alpha-amylase (imp
15	1084	39.9	494	1 B45738	alpha-amylase (EC
16	1072	39.4	494	2 AD0751	cytoplasmic alpha-
17	1071	39.4	495	2 B90962	cytoplasmic alpha-
18	1064	39.1	495	1 A45738	alpha-amylase (EC
19	1052	38.7	495	2 B85810	cytoplasmic alpha-
20	379.5	14.0	217	2 A19506	alpha-amylase (EC
21	327	12.0	1196	2 S21130	beta-amylase (EC 3
22	322.5	11.9	482	2 S31478	alpha-amylase (EC
23	301.5	11.1	421	2 S10514	alpha-amylase (EC
24	288	10.6	423	2 T09942	alpha-amylase (EC
25	274.5	10.1	440	2 S14958	alpha-amylase (EC
26	271	10.0	428	2 T05521	alpha-amylase (EC
27	271	10.0	504	2 A55861	alpha-amylase (EC
28	269	9.9	826	2 E36720	probable alpha-amyl
29	268.5	9.9	547	2 A32803	glucan 1,4-alpha-m

ALIGNMENTS

RESULT 1

A27705 alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase

C;Species: Bacillus sp.

C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

C;Accession: A27705

R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.

Biochem. Biophys. Res. Commun. 151, 25-31, 1988

A;Title: Nucleotide sequence of the maltotetraose-producing amylase gene from an alkaloph

A;Reference number: A27705; MUID:88162814; PMID:3258152

A;Accession: A27705

A;Molecule type: DNA

A;Residues: 1-518 <TSU>

A;Cross-references: GB:M18862; NID:g142496; PIDN:AAA22231.1; PID:g142497

A;Experimental source: chromosomal DNA of strain 707

A;Note: amino end of mature protein also determined

C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F;1-33/Domain: signal sequence #status predicted <SIG>

F;34-518/Product: alpha-amylase #status experimental <MAT>

F;236-369/Domain: alpha-amylase core homology <AMY>

F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted

F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 88.8%; Score 2414; DB 1; Length 518;

Best Local Similarity 86.2%; Pred. No. 2.4e-157;

Matches 418; Conservative 33; Mismatches 34; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLPN...DASNLNRNGITAIWIPPAWKQTSQNDVGGA 60

Db 34 HHNGTGTMMQYFEWHLPN...DASNLNRNGITAIWIPPAWKQTSQNDVGGA 93

Qy 61 YDLYDLGEFQKQGVTRTKYGRSQLESIAHALKNGVQVYGVVVVNNHKGADATENVLAV 120

Db 94 YDLYDLGEFQKQGVTRTKYGRSQLOAAVTSLNKNGIQVYGVVVVNNHKGADATEMVRV 153

Qy 121 EVNPNRNRQELSGYTTTEATWKTFDPGNGNTYSDFKRWHTFDGVDWDSQSFQNRYYKF 180

Db 154 EVNPNRNRQELSGYTTTEATWKTFDPGNGNTYSDFKRWHTFDGVDWDSQSFQNRYYKF 213

Qy 181 RGDGKADWEVDSENGVYDYLMDVMDHPVNVNLRNGEWTNTNLIDGFRIDAVKH 240

Db 214 RGHGKADWEVDSENGVYDYLMDVMDHPVNVNLRNGEWTNTNLIDGFRIDAVKH 273

Qy 241 IKYSFTFDLWLTNRNATGKEMFAVEAFWKNLDGALENYLNKTNWNSHVSFVDFPLHLYNA 300

Db 274 IKYSFTFDLWLTNRNATGKEMFAVEAFWKNLDGALENYLNKTNWNSHVSFVDFPLHLYNA 333

Db 390 VFYGDYMGTTGDSQREIPALKKHKEIPILKARKQVAYGAQHDYFPHHDIVGWTRREGDSVA 449
QY 423 NSGLATIMSDPGGKWMYQKAGQWHDITGNKFGTWTINADGWANFVSGSVSIW 482
Db 450 NSGLAALITDGPCKAKMYGVRQAGETWHDITGNRSEPVVINSEGFEHVNGSVSIY 509
QY 483 VKR 485
Db 510 VQR 512

RESULT 3
A24549
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24549; I39501; I39770
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: A24549
A;Molecule type: DNA
A;Residues: 1-549 <GRA>
A;Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513
A;Experimental source: Genomic DNA of strain NZ-3
R;Satoh, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A;Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distant
A;Reference number: I39501; MUID:08139156; PMID:3257753
A;Accession: I39501
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RES>
A;Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478
A;Experimental source: strain DY-5
A;Accession: I39770
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RE2>
A;Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A;Experimental source: strain 799
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.4%; Score 1888.5; DB 1; Length 549;
Best Local Similarity 67.7%; Pred. No. 2e-121;
Matches 325; Conservative 74; Mismatches 80; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRGITAIPPAWKGTSONDVGAYDLYD 65
Db 39 NGTMMQYFEWHLPPDGTGLTKVANEANLSLIGTALWLPAYKGTSRSDVGAYDLYD 98
QY 66 LGFENQKGTVRTKGTGRSQALESALHAKNNGVQVYGDVVMNHKGGADATENVLAVENPN 125
Db 99 LGFENQKGTVRTKGTGRKQAYIQALQAAHAGMAYADVDFHKGADGETWDAVENPS 158
QY 126 NRNOEISGDYITAEWTKDFPFGKNTYSDFKRWYHFDGVDWDSQROFQNRRIYKFRGDGK 185
Db 159 DRNOEISGTQIQAWTKDFPFGKNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217

QY 186 AWDWEVDSENGYDLYMAYADVMDMDHPEVAVNELRWGEMWYNTNLNDGFRIDAVKHIXSF 245
Db 218 AWDWEVDTEGNGYDLYMAYADLMDHPEVAVTELKMWGKMYNTNTIDGFRIDAVKHIXSF 277
QY 246 TRDWLTHVRNATGEMFAVAFKNDLGALENLKNKTNHNSVDFVPLHYNLYNASGG 305
Db 278 FPDWLSYVRSQTGKPLFTVGEYSYDINKLHNITKTNGTMSLFDAPLHKKFYTASGG 337
QY 306 NYDMAKLLNGTIVQKHMPHMAVTVDNHDSPGSELESFVQEWFKPLAYALILTREGNTHPNSG 425
Db 398 VFYGDYMGTTGDSQREIPALKKHKEIPILKARKQVAYGAQHDYFPHHDIVGWTRREGDSVA 457
QY 426 LATIMSDPGGKWMYQKAGQWHDITGNKFGTWTINADGWANFVSGSVSIWVKR 485
Db 458 LAALITDGPCKAKMYGVRQAGETWHDITGNRSEPVVINSEGFEHVNGSVSIY 517

RESULT 4
A54541
Alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI792)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C;Accession: A54541
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A;Reference number: A54541
A;Molecule type: DNA
A;Residues: 1-549 <JOR>
A;Cross-references: GB:X59476
A;Experimental source: chromosomal DNA of strain DNI792
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.4%; Score 1887.5; DB 1; Length 549;
Best Local Similarity 67.5%; Pred. No. 2.4e-121;
Matches 324; Conservative 74; Mismatches 81; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWHLPNDDGNHNRRLRDDASNLNRGITAIPPAWKGTSONDVGAYDLYD 65
Db 39 NGTMMQYFEWHLPPDGTGLTKVANEANLSLIGTALWLPAYKGTSRSDVGAYDLYD 98
QY 66 LGFENQKGTVRTKGTGRSQALESALHAKNNGVQVYGDVVMNHKGGADATENVLAVENPN 125
Db 99 LGFENQKGTVRTKGTGRKQAYIQALQAAHAGMAYADVDFHKGADGETWDAVENPS 158
QY 126 NRNOEISGDYITAEWTKDFPFGKNTYSDFKRWYHFDGVDWDSQROFQNRRIYKFRGDGK 185
Db 159 DRNOEISGTQIQAWTKDFPFGKNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
QY 186 AWDWEVDSENGYDLYMAYADVMDMDHPEVAVNELRWGEMWYNTNLNDGFRIDAVKHIXSF 245
Db 218 AWDWEVDTEGNGYDLYMAYADLMDHPEVAVTELKMWGKMYNTNTIDGFRIDAVKHIXSF 277
QY 246 TRDWLTHVRNATGEMFAVAFKNDLGALENLKNKTNHNSVDFVPLHYNLYNASGG 305

Db 278 FPDWLSVRSQTKPLFTVGEYWSYDINKLHNYITKDTGMSLFDAPLHNKFTASKSGG 337
QY 306 NYDMAKLINGTVVQKHPMAHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRQGYPS 365
Db 338 AFDMRTLMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQGYPC 397
QY 366 VFYGDYVIGPHTSVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTHPNSSG 425
Db 398 VFYGDYVIGPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKPGSG 457
QY 426 LATIMSDPGGKWMYVQNKAGQVWHDTGNKPGVTITNADGWANFSVNGSVSIWVKR 485
Db 458 LAALITDGGSGKWMYVQKHAGKVFYDLTGNSRSDTVTINSDDGKFKVNGSVSVWVPR 517
RESULT 5
A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; PMID:85234394; PMID:3924897
A;Reference number: A24436
A;Molecule type: DNA
A;Residues: 1-549 <NAK>
A;Cross-references: GB:M11450
A;Experimental source: plasmid pAT5
A;Note: amino end of the mature protein also determined
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39777
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-45 <RES>
A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Gene: amyS
A;Genome: plasmid
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted
Query Match 69.1%; Score 1880.5; DB 1; Length 549;
Best Local Similarity 67.5%; Pred. No. 7.1e-121;
Matches 324; Conservative 72; Mismatches 83; Indels 1; Gaps 1;
QY 6 NGTMMQYFEWHLPNDRGNHNRLLDASLNRRGITAIWPPAWKGTQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWHLPPDDGLTWTKVANEANLSSGLITALLWLPAYKGTSRSDVGVGYDLYD 98
QY 66 LGBFNKGTVRTKYGTRQSLESIAHLKNGVGVYGDVVMNHHKGGADATENVLAVENPN 125
Db 99 LGBFNKGAVRTKYGTKAQVLOAIQAHAAGMQVADVVPFDHKGAGDTEWVDVAVENPS 158
QY 126 NRNQETISGDYTIKAWTKKPPGRGNTYSPDKFWYHFDGVDWDSRQFQNRIRYKFGDGK 185
Db 159 DRNQETISGTYQIQAWTKFDPGRGNTYSPDKFWYHFDGVDWDSRKL-SRIIYKFGIGK 217
QY 186 AWDWEYDSENGNYDILMYADVDMDHPVNVNLRNRRGEWYTNLTNLNLDGFRIDAVKHIKYSF 245

Db 218 AWDWEYDTENGNYDILMYADVDMDHPVNVNLRNRRGEWYTNLTNLNLDGFRIDAVKHIKYSF 277
QY 246 TRDWLTHVRNATCKEMFAVAFWKNDLGALENLKNKTNNHNSVFDPLHVLNLYNASSG 305
Db 278 FPDWLSVRSQTKPLFTVGEYWSYDINKLHNYITKDTGMSLFDAPLHNKFTASKSGG 337
QY 306 NYDMAKLINGTVVQKHPMAHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRQGYPS 365
Db 338 FPDWLSVRSQTKPLFTVGEYWSYDINKLHNYITKDTGMSLFDAPLHNKFTASKSGG 397
QY 366 VFYGDYVIGPHTSVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTHPNSSG 425
Db 398 VFYGDYVIGPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKPGSG 457
QY 426 LATIMSDPGGKWMYVQNKAGQVWHDTGNKPGVTITNADGWANFSVNGSVSIWVKR 485
Db 458 LAALITDGGSGKWMYVQKHAGKVFYDLTGNSRSDTVTINSDDGKFKVNGSVSVWVPR 517
RESULT 6
ALASN
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amylioliquefaciens
C;Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A92389; A9307; I39756; I39763; A00843
R;Takinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
J. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced fr
A;Reference number: A92389; MUID:83108808; PMID:6185474
A;Contents: PUB110
A;Accession: A92389
A;Molecule type: DNA
A;Residues: 1-514 <TAK>
A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA2211
R;Chung, H.S.; Friedberg, F.
Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.
A;Reference number: A9307; MUID:80241725; PMID:6156671
A;Accession: A9307
A;Molecule type: protein
A;Residues: 32-53,'I',55-63,'I',65-78,'D',80-83,'S',85-222 <CHU>
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of th
A;Reference number: I39756; MUID:82051296; PMID:6170539
A;Accession: I39756
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.
Gene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its ow
A;Reference number: I39763; MUID:88137952; PMID:2830166
A;Accession: I39763
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-39 <RE2>
A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-362/Domain: alpha-amylase core homology <AMY>
F;133,231,266/Binding site: calcium (Asp, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
Query Match 68.8%; Score 1871; DB 1; Length 514;

Best Local Similarity 67.9%; Pred. No. 2.9e-120;
Matches 330; Conservative 65; Mismatches 87; Indels 4; Gaps 2;

QY 3 NGTNGTMVQFYFWHLPNLNDGNHNRRLRDDASNLNRRGITAIIWIPPAWKGTISQNDDVGYCAYD 62
 :
Db 30 SAVNGTLMOIFYFMYTPNDGGQHWRKLQDAEHSLDIGITAWIIPPAYKGLSQSDNGYGPD 89

QY 63 LYDLGEFNKGTVRTKYTGTSQSLESAIHAKNNGVQVGYDVNMHHKKGDATENVLADEV 122
 :
Db 90 LYDLGFQQKTVRTKYTKSLSQLAIGSLHSRNVOVGYDWLNHRKAGADATEDVTAVEV 149

QY 123 NPNRNRQEISGDYTIEAWTKFDPGRGNTYSDFKWRYHPDGVDWDQSFQRNQRIYVKFG 182
 :
Db 150 NPANRNQETSEETQIKAWTDPRFPGRNTYSDPKRWHYHFPGADWDERSKI-SRIIFRG 208

QY 183 DGKAWEDEVSNGENDYLAMYADVMDPHVPVNELRWGEWYYTNLLDGLFRIDAVKHJK 242
 :
Db 209 EGKAWEDEVSNGENDYLAMYADVMDPHVPVAETKKGIWYNELSGLDGFRIIDAACHIK 268

QY 243 YSTTRDWLTIVRNATGEMFAVAFKNKDILGALENLYNKTNWHSHSPDVDPLHNLYNASN 302
 :
Db 269 FSELRDVVQVRQTGKMFTVAEYMWNNAKGLNYLNKTSFNQSVFDVPLENFLOQAASS 328

QY 303 SGGNYDMAKLLNGTVTQOKPMPHVATTVDNHDSQPGESLESFOVEWPKPALAYAILTREOG 362
 :
Db 329 QGGYDMRRLDGTVSRHPEKAVTFVENHDTPQGSLVESTVQTWFKPALAYAILFRESG 388

QY 363 YPSVFYGDYGIPTHS---VPAMKAKIIDPILEARONPAYGTOHYDFDHNIIGWTTREGNT 419
 :
Db 389 YPVFFYGMVGTGKTSPEKPSLKDNIEPIHKARKEYAGPQHDYIDHPDIVGWTTREGBS 448

QY 420 THPNSGLATIMSGPGGCKMVMYQONKAGOVWHDITCNKPGTDTINADGANFNVNGGSV 479
 :
Db 449 SAASKSGLAALTIDPGCGSKRMVAGLNAGETWYDIICNRSDITVKIGSDCWGEFHVNDGSV 508

QY 480 SIWVKR 485
 |
Db 509 SIWVKR 514
 |:

RESULT 7

ALBSF

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DY-5) plasmid
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 16-Feb-1997
C;Accession: A91999; B91999; J91804; A00845
R;Thara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Udaoka, S.
J. Biochem. 98, 95-103, 1985
A;Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology betw
A;Reference number: A91999; UID:86008166; PMID:3876333
A;Accession: A91999
A:Molecule type: DNA
A;Residues: 1-548 <IR>
A;Cross-references: GB:X02769
A;Experimental source: Plasmid phi300 from strain DY-5
A;Accession: B91999
A:Molecule type: protein
A;Residues: 35-48 <IR>
A;Experimental source: strain DY-5
R;Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,
J. Bacteriol. 164, 1182-1187, 1985
A;Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pri
A;Reference number: A91804; UID:86059211; PMID:2999073
A;Contents: pBRM101
A;Accession: A91804
A:Molecule type: DNA
A;Residues: 1-29,'Q','31'-75,'w',77-122 <TSU>
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Genome: plasmid
A;Start codon: GTG
C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide 6-phosphatase; alpha-amylase
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-548/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.8%; Score 1816; DB 1; Length 548;
Best Local Similarity 66.0%; Pred. No. 1.8e-116;
Matches 317; Conservative 71; Mismatches 90; Indels 2; Gaps 2;

Qy 6 NGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWTPPAWKGTSONDVGYGADLYD 65
Db 39 NGTMMQYFEWYLPDDGTLTKVANEANNLSLIGTALSPLPYPAYKGTSRSDVGYYDLYD 98
Qy 66 LGBFNKGTVRTKYGTRFSQLESIAHAIKKNQGVQYGDVVMNHKGGADATENVLAVENPN 125
Db 99 LGBFNKGTVRTKYGTYKAQYLQAIQAHAAGQVYADVDFDHKGGADGTETWDAVENPS 158
Qy 126 NRNQEISGDTYTBWTKFPFPGRGNTSYDPKRWYHFDGVDMQSQRFQNRYYKFRGDGK 185
Db 159 DRNQEISGTYQIQWTKFPFPGRGNTSYSPKRWYHFDGVDMQSQRFQNRYYKFRGIGK 217
Qy 186 ANDWEVDSENGYDLYMADVMDHPEVNVNELPRGCEWYTNLNDGFRIDAVKHIKYSF 245
Db 218 ANDWEVDTEGNYDLYMADLMDHPEVNVTELKNQWKYVNTNIDGFRDLGLKHIKPSF 277
Qy 246 TRDLWTHVRNATGKEMFAVAEFWKNDLGALENLYLNKTNWNHVSFVDFPLHYNLYNASNSGG 305
Db 278 FPDLSYVSRSQTKPLFTGVEYSYDINKLHVITKTNGTMSLFDAPLHNKFYASKSGG 337
Qy 306 NYDMAKLINGTVVQKHMPHMAVTFVDNHDSPGSELSFVQEWPKPLAYALILTREGQYPS 365
Db 338 AFDMTLMTNLTMKDQPTLAVTFVDNHDNTNPAKRC-SHGRPWPKPLAYAFILTRQEGYPC 396
Qy 366 VFYGDYVYGTPHSVPAMKAKIDPILEARONFANGTQHDYFDHNIIGWTRGNTHTPNSG 425
Db 397 VFYGDYVYGTPHSVPAMKAKIDPILEARONFANGTQHDYFDHNIIGWTRGNTHTPNSG 456
Qy 426 LATIMSDPGGKEMTVGVQNKAGVMDHITGNKPGVTINADGWANFVNGSGSVSWVKR 485
Db 457 LAALITDGAGRSKWMYVQKHAGKVFYDLTGRESDTVTINSDGWGEFKNGSGSVSWVVR 516

RESULT 8
S15713
Alpha-amylase (EC 3.2.1.1) - Bacillus circulans
C;Species: Bacillus circulans
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S15713
R;Marcel, T.
submitted to the EMBL Data Library, May 1991
A;Reference number: S15713
A;Accession: S15713
A;Molecule type: DNA
A;Residues: 1-493 <WAR>
A;Cross-references: EMBL:X60779; NID:g39411; PIDN:CAA43194.1; PID:g39412
C;Genetics:
A;Gene: amyE
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;200-333/Domain: alpha-amylase core homology <AMY>

Query Match 50.5%; Score 1373; DB 2; Length 493;
Best Local Similarity 51.3%; Pred. No. 2.9e-86;
Matches 245; Conservative 81; Mismatches 150; Indels 2; Gaps 2;

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QY 6 NGTMMQYFEWHLFNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65
Db 4 NHTMMQYFEWHLAAGDGHKRLAEMAPELKAGDITVWVPVTKAVSAEDTGGYGYDLYD 63
QY 66 LGFENQKGTVRTKYGTRSQLESALHALKNGNGVQYGVDMVNNHKGADATENVLAVENPN 125
Db 64 LGFEDQKGTVRTKYGTRKQELIEIAECQKNGIAYVVDLVNHNKAGADETEVFKVIEDPN 123
QY 126 NRNOISGDTYTEAWTKFDPFGRGNTYSDFKRWYHFDGVDWQDSROFQNRVYKFRGDGK 185
Db 124 DRTKEISEPFEIEGWTKTFPGRGDQYSSFKWNSEHFGTDFD-AREERTGVFRIAGENK 182
QY 186 AWDWEVDSENGNDYLMYADVMDHDPVNNELRRWGEWYNTNLNDGFRIDAVKHICYSP 245
Db 183 KWNENVDSENGNDYLMYADVMDHDPVNNELRRWGEWYNTNLNDGFRIDAVKHICYSP 242
QY 246 TRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHNSVDFVPLHYNLYNASNG 305
Db 243 IKFAFAMIRKRGQDFYVGFGEFWNSLDACREELDTVDYQIDFVSLHYKLHEASLKR 302
QY 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILTREOGYPS 365
Db 303 DFDLSKIFDUTLQVTHAVTFVDNHDSPHEALESWIGDWKPKSAYALTLLRRDGPV 362
QY 366 VFYGDYGI-PTHSVPAWMAKIDPILLEARONFAYGTHQDYPDHNNIGTWREGNTTHPS 424
Db 363 VFYGDYGI-PTHSVPAWMAKIDPILLEARONFAYGTHQDYPDHNNIGTWREGNTTHPS 422
QY 425 GLATIMSDGPGGKMWYVQKQAGVWHDTGNKPGTVTINADGWANFSVNGSGSVI 482
Db 423 GCAVVISGDDGKRMFGEHRAGEVWVDLTKSCDDQITIEEDGMAFHVCGGGSVW 480

RESULT 9
G95160
alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: G95160
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eelsen, J.A.; Read, T.D.; Peterson, S.; Heid
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95160
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
C:Gene: Spi382
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 46.6%; Score 1267; DB 2; Length 484;
Best Local Similarity 49.0%; Pred. No. 4.9e-79;
Matches 235; Conservative 77; Mismatches 162; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWHLFNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65
Db 3 NQTLAQYFEWYLPDGHQWTRLAENAPHLAHLGISHVWMPAPKATNEKXDVGVGYDLYD 62
QY 66 LGFENQKGTVRTKYGTRSQLESALHALKNGNGVQYGVDMVNNHKGADATENVLAVENPN 125
Db 63 LGFENQKGTVRTKYGFKEDYLOAIQALKAQGIQPMADVVLNHNKAAADHREAFQVIEVDV 122
QY 126 NRNOISGDTYTEAWTKFDPFGRGNTYSDFKRWYHFDGVDWQDSROFQNRVYKFRGDGK 185
Db 123 DRTVLEGPFTINGWTSFTFDGQDITYGFHWHHTFTGTDYDAKES--KSGIYLQGDNK 181
QY 186 AWDWE--VDSENGNDYLMYADVMDHDPVNNELRRWGEWYNTNLNDGFRIDAVKHICY 243
Db 183 KWNENVDSENGNDYLMYADVMDHDPVNNELRRWGEWYNTNLNDGFRIDAVKHICY 242
QY 246 TRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHNSVDFVPLHYNLYNASNG 305
Db 243 IKFAFAMIRKRGQDFYVGFGEFWNSLDACREELDTVDYQIDFVSLHYKLHEASLKR 302
QY 306 NYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILTREOGYPS 365
Db 303 DFDLSKIFDUTLQVTHAVTFVDNHDSPHEALESWIGDWKPKSAYALTLLRRDGPV 362
QY 366 VFYGDYGI-PTHSVPAWMAKIDPILLEARONFAYGTHQDYPDHNNIGTWREGNTTHPS 424
Db 363 VFYGDYGI-PTHSVPAWMAKIDPILLEARONFAYGTHQDYPDHNNIGTWREGNTTHPS 422
QY 425 GLATIMSDGPGGKMWYVQKQAGVWHDTGNKPGTVTINADGWANFSVNGSGSVI 482
Db 423 GCAVVISGDDGKRMFGEHRAGEVWVDLTKSCDDQITIEEDGMAFHVCGGGSVW 480
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Db 182 GWANEELVDNENGYDLYADLDFKHPEVIQNIYDWADWFMETTTGVAGFRDLAVKHIDS 241
QY 244 SFTRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHNSVDFVPLHYNLYNASNG 303
Db 242 FFRNFIIRDMKEKYGDDFVVFGEFNPDKBANUDYLEKTEEHFDLVDVRLHQLNFEASQA 301
QY 304 GGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILTREOGY 363
Db 302 GANYDLRGIFTDSLVELKPKDPAVTVDNHDTRGQALESTVEEMFKPAAYALILLRQDGL 361
QY 364 PSVFGDYGYIP-THSVPAWMAKIDPILLEARONFAYGTHQDYPDHNNIGTWREGNTTHP 422
Db 362 PCVFGDYGYISQYQAQEDFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVRASG--AEN 419
QY 423 NSGLATIMSDGPGGKMWYVQKQAGVWHDTGNKPGTVTINADGWANFSVNGSGSVI 482
Db 420 QSPIAVLIISNDQENSKSMFVGQEWNTQTTFVDLLGNHQQGVTTIDEEGYGQFPVSARSVW 479

RESULT 10
F98026
alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: F98026
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98026
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK00043.1; PID:g15458876; GSPDB:GN00174
C:Genetics:
C:Gene: amy
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase

Query Match 46.5%; Score 1265; DB 2; Length 484;
Best Local Similarity 48.8%; Pred. No. 6.7e-79;
Matches 234; Conservative 79; Mismatches 161; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWHLFNDGNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGAYDLYD 65
Db 3 NQTLAQYFEWYLPDGHQWTRLAENAPHLAHLGISHVWMPAPKATNEKXDVGVGYDLYD 62
QY 66 LGFENQKGTVRTKYGTRSQLESALHALKNGNGVQYGVDMVNNHKGADATENVLAVENPN 125
Db 63 LGFENQKGTVRTKYGFKEDYLOAIQALKAQGIQPMADVVLNHNKAAADHREAFQVIEVDV 122
QY 126 NRNOISGDTYTEAWTKFDPFGRGNTYSDFKRWYHFDGVDWQDSROFQNRVYKFRGDGK 185
Db 123 DRTVLEGPFTINGWTSFTFDGQDITYGFHWHHTFTGTDYDAKES--KSGIYLQGDNK 181
QY 186 AWDWE--VDSENGNDYLMYADVMDHDPVNNELRRWGEWYNTNLNDGFRIDAVKHICY 243
Db 182 GWANEELVDNENGYDLYADLDFKHPEVIQNIYDWADWFMETTTGVAGFRDLAVKHIDS 241
QY 244 SFTRDWLTHVRNATKEMFAVAEFWKNDLGALENLYNKTNWNHNSVDFVPLHYNLYNASNG 303
Db 242 FFRNFIIRDMKEKYGDDFVVFGEFWNKDKEANLDYLEKTEEHFDLVDVRLHQLNFEASQA 301
QY 304 GGNYDMAKLLNGTVVQKHPMHAVTFVDNHDSPGESLESFVQEWFKPLAYALILTREOGY 363
Db 302 GANYDLRGIFTDSLVELKPKDPAVTVDNHDTRGQALESTVEEMFKPAAYALILLRQDGL 361
QY 364 PSVFGDYGYIP-THSVPAWMAKIDPILLEARONFAYGTHQDYPDHNNIGTWREGNTTHP 422
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Db 362 PCVFYGYGYSQYAOQDPKEILDRLLAIRKDLAYGEQNDYFPHANCIGWVRSG--AEN 419
Qy 423 NSGLATIMSDPGGKEMVYQGNKAGQVWHIDITGNKPGTGTVINADGWANFVNGSVSIW 482
Db 420 QSPIAVLISNDQENSKSMFVQEWNTQTFVDLLSHQGVQVITDEBGYQGPVSARSVSW 479
RESULT 11
AH2079
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-492 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA073889.1; PID:g17131281; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Gene: alr2190
C;Genetics:
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
Query Match 45.8%; Score 1245; DB 2; Length 492;
Best Local Similarity 48.1%; Pred. No. 1.6e-77;
Matches 236; Conservative 84; Mismatches 155; Indels 16; Gaps 5;
Qy 6 NGTMMQYFEWHLPNDCNHNRLRDDASNLNRGITAIPPAWKGTSON-DVGYGAYDLY 64
Db 5 NGTMMQYFHWIIPNDGNLNSKVEASAPELADAGTAMWLPAYKGFAGSDVGYGVYDLF 64
Qy 65 DLGEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVGVYVNMHKGADATENVLAVENP 124
Db 65 DLGEFDQKGSVRTKYGTRQYLDVAVKSLQTHGLQVYADAVLNHKGGDVAVETPKATPPQ 124
Qy 125 NNRNQEISGDIYIEAWTKFPFGNGTYSDFKRWYHFDGVWDQSQFQNRIFYKRGDG 184
Db 125 DDRLNPKGGLQDIKTYTHYNNPGRQGYKSNPEWHWHFDDAVDYNEYS-GDRSTVYLLE 183
Qy 185 KAMDWEVDSNGYDLYMADVMDHPVNNELRWGEWYTNLNLGFRIDAVKHIKYS 244
Db 184 KNFDYVALEKGNFAYLWGCDDLDFQNEWVRGEVTVYWKWCLDTTKVDGFRIDAIKHISTW 243
Qy 245 FTRDLWTHVRNATGKEMFAVAEFWKNLGDALENYLNKTNWNHVSFVDPVPLHNLNNA 304
Db 244 FFPWIDALEBHAGKDLFMVGEYWNIDNTLLWTVDVAVGKMSVDFVPLHYNFHOAKSG 303
Qy 305 GNYDMAKLLNGTVVQKHPHIAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRQGY 364
Db 304 GNYDMRILDTGMQORPHTAVTFVENHDSQPLQALSVBEPFKPLAYAILLRQEGYP 363
Qy 365 SVFQDYGYGTPHS-----VPAMKAKIDPILAEARONFAYGTOHDYFDHNNIGW 413
Db 364 CVFHADYGYGAEYEDWGDGKNRYNIFMPSHRWIIDKLLYARKHYAGPYQNYLDHWNIGW 423
Qy 414 TREGNTTHPSGLATIMSDPGGKEMVYQGNKAGQVWHIDITGNKPGTGTVINADGWANF 473
Db 424 TRLGDAHP-OGMAVIMVSDGSEGIKWEVGV--KNTKFDITUTEHKEAVYTNWGWGEFR 480
Qy 474 VNGGSVSIWVK 484
Db 481 CLGGSVSVWVQ 491
RESULT 12
C86781
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: C86781
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissbach, J.; Ehrlich,
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86781
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-491 <STO>
A;Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
Query Match 42.08%; Score 1143; DB 2; Length 491;
Best Local Similarity 42.8%; Pred. No. 1.5e-70;
Matches 205; Conservative 104; Mismatches 166; Indels 4; Gaps 3;
Qy 8 TMMQYFEWHLPNDCNHNRLRDDASNLNRGITAIPPAWKGTSON-DVGYGAYDLYDL 66
Db 3 TILQAFWYLPSSQHNWNIKENIPDLCKLFGSLWLPASKASGVEDVGYGYTDLFDL 62
Qy 67 GEFNQKGTVRTKYGTRSQLESIAHALKXNGVQVGVYVNMHKGADATENVLAVENP 126
Db 63 GEFQKGTIPTKYGTRKDEYLDLINTLHNNIEVYADIVFNHMGADETETIADIKAE 122
Qy 127 RNRNQEISGDIYIEAWTKFPFGNGTYSDFKRWYHFDGVWDQSQFQNRIFYKRGDG 186
Db 123 HLHNIENKKTVEWTKFTFFGRQGYKDYNIWTHNFTGIDYDE-RKNQEBILEF--EG 179
Qy 187 WDNEVDSNGYDLYMADVMDHPVNNELRWGEWYTNLNLGFRIDAVKHIKYSFT 246
Db 180 WDNEVDSNNFVYLMGADLDFSVSEIVQELKWHFSEWTKIDGFRDAIKHIDPKYP 239
Qy 247 RDMLTVRNATGKEMFAVAEFWKNLGDALENYLNKTNWNHVSFVDPVPLHNLNNA 306
Db 240 DKWLEQRAKDLRKLFTVGEVWSDDLKLEYLEQSSDRIQLFDVPLHFNKKEAS 299
Qy 307 YDMAKLLNGTVVQKHPHIAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRQGY 366
Db 300 FDMRTLFDHTLITASQPELSVTFVDNHDTPQEQALQSWIPAWFKHAYSLILRRKKTPT 359
Qy 367 FYGDYGYGTPHSVPAMKAKIDPILAEARONFAYGTOHDYFDHNNIGWTRGNTTHP 426
Db 360 FWGLYGIPTSHNNVPGDNLRTMIALRKSEFURENDYFDHPDILIGWNTILKIDN 419
Qy 427 ATMSDGPGEKMWYVQGNKAGQVWHIDITGNKPGTGTVINADGWANFVNGGSVSIW 485
Db 420 SCILTNKNGSKYMIIDKAYAGVYIDLFGHHEIPITLDQNGGAFFVNDGVSVMVDK 478
RESULT 13
G98247
cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacteri
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: G98247
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G98247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L1863
A;Map position: linear chromosome

C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.6%; Score 1104; DB 2; Length 506;
Best Local Similarity 44.0%; Pred. No. 7e-68;
Matches 218; Conservative 83; Mismatches 176; Indels 18; Gaps 6;

QY 3 NGTNGTMQYFEWHL PNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSON-DVGYGAY 61
DB 11 NMAGRTLLQFFHYYPDGKGLWSEVAEKAESLAKMGITDVLPPAYKGAAGGSVGYDY 70
QY 62 DLYDLGFGNOKGTVTKYGRSQALESIAHLKKNNGVQVGVVNNHKGADATENVLAVE 121
DB 71 DLFDLGEFGDKGTATYKIDRAALEHAGKTUKONGIRVIHVVNHNKMGADAEKVRVR 130
QY 122 VFNPNRNOEISGDYITIEAWTKFDPFGRGNTYSDFKRWYHFDGVDM--DQSRQFQNR 179
DB 131 VNPDRDIDDEPPALAYTRFTFPGNGKHSKFIWDLKCFSGVDHIEEPTDGI 190
QY 180 FRGDKAWDEVDSENGNYDLYMADVMDHPVNNELRWGEWYNTNLNDGRIDAVK 239
DB 191 EYGDGE-WNEEVDQENGFDYLMGADVFEFRNRAVYEELKYWRWLSQVQVDFRLDA 249
QY 240 HIKYSFRDLWLTVRNATGKEMFAVAFWKNLGALENLKNNTNHNHVSFVDPVPLH 299
DB 250 HIRAFPRDVGWHRETVDPLFVVAEYHWPDLKLSYLELVYDKQLMLFDVALH 309
QY 300 ASNSGGNYDMKLLNGTVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALIL 359
DB 310 ASKQGGDFMRSIFDGLSVSAVDPHATVLDVNDHTQPLQSLAPVPEWFKPLAYA 369
QY 360 EQYPSVFGDYGYIP-----THSVPAWKAKIDPILBARQNFAYGTQHDYFDH 408
DB 370 EGVPCVFPDLFGTSYTDGTGNGNEYKIDIPATEC-LPKLIEARSRFANGPQTD 428
QY 409 NIIGTWRENTTHPNSGLATIMSDGPGGKMWYGVQNKAGOVVHDTGNKPGVTIN 468
DB 429 SCIAFIRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHRE 486
QY 469 WANFVSNGGSVSIWV 483
DB 487 KGTFTPNGGSVSVWV 501

RESULT 14
AD3038
A:Title: alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AD3038
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AD3038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAI44722.1; PID:gl7742354; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: amyA

A:Map position: linear chromosome
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
Query Match 40.6%; Score 1103; DB 2; Length 495;
Best Local Similarity 44.3%; Pred. No. 8e-68;
Matches 217; Conservative 83; Mismatches 172; Indels 18; Gaps 6;

QY 8 TMMQYFEWHL PNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSON-DVGYGAYDYL 66

DB 5 TLLQFFHYYPDGKGLWSEVAEKAESLAKMGITDVLPPAYKGAAGGSVGYDYDLFDL 64
QY 67 GFENOKGTVTKYGRSQALESIAHLKKNNGVQVGVVNNHKGADATENVLAVEVNP 126
DB 65 GEPDQGTATYKIDRAALEHAGKTUKONGIRVIHVVNHNKMGADAEKVRVRVP 124
QY 127 RNOEISGDYITIEAWTKFDPFGRGNTYSDFKRWYHFDGVDM--DQSRQFQNR 184
DB 125 RTDIDDEDPPALAYTRFTFPGNGKHSKFIWDLKCFSGVDHIEEPTDGI 184
QY 185 KAWDEVDSENGNYDLYMADVMDHPVNNELRWGEWYNTNLNDGRIDAVK 244
DB 185 E-WNEEVDQENGFDYLMGADVFEFRNRAVYEELKYWRWLSQVQVDFRLDA 243
QY 245 FTRDLWLTVRNATGKEMFAVAFWKNLGALENLKNNTNHNHVSFVDPVPLH 304
DB 244 FRDWGWHRETVDPLFVVAEYHWPDLKLSYLELVYDKQLMLFDVALH 303
QY 305 GRYDMAKLLNGTVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALIL 364
DB 304 GDFMRSIFDGLSVSAVDPHATVLDVNDHTQPLQSLAPVPEWFKPLAYA 363
QY 365 SVFYGDYGYIP-----THSVPAWKAKIDPILBARQNFAYGTQHDYFDH 413
DB 364 CVFYPDLPFGTSYTDGTGNGNEYKIDIPATEC-LPKLIEARSRFANGPQTD 422
QY 414 TRENTTHPNSGLATIMSDGPGGKMWYGVQNKAGOVVHDTGNKPGVTIN 473
DB 423 IRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHRE 480
QY 474 VNGGSVSIWV 483
DB 481 TNGGSVSVWV 490

RESULT 15

B45738
A:Title: alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Salmonella typhimurium
C:Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: B45738
R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A:Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A:Reference number: A45738; PMID:93015717; PMID:1400215
A:Accession: B45738
A:Molecule type: DNA
A:Residues: 1-494 <RAH>
A:Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045
C:Genetics:
A:Gene: amyA
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F:202-335/Domain: alpha-amylase core homology <AMY>
F:239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.9%; Score 1084; DB 1; Length 494;
Best Local Similarity 42.5%; Pred. No. 1.6e-66;
Matches 209; Conservative 83; Mismatches 182; Indels 18; Gaps 6;

QY 6 NCTMMQYFEWHL PNDGNHNRRLDDASNLNRGITAIIWIPPAWKGTSON-DVGYGAYDYL 64
DB 3 NPTLLQYFHHYYPDGKGLWSELAERADGLNDGINVMWLPACKGASGGSVGYDYD 62
QY 65 DLGEFNOKGTVTKYGRSQALESIAHLKKNNGVQVGVVNNHKGADATENVLAVE 124
DB 63 DLGEFDQGTATYKIDRAALEHAGKTUKONGIRVIHVVNHNKMGADAEKVRVR 122

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FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 240 240 CALCIUM 2 (BY SIMILARITY).
FT METAL 242 242 CALCIUM 2 (BY SIMILARITY).
FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
  Query Match 88.8%; Score 2414; DB 1; Length 518;
  Best Local Similarity 86.2%; Pred. No. 1.4e-155;
  Matches 418; Conservative 33; Mismatches 34; Indels 0; Gaps 0;
QY 1 HHNGTNGTMMQYFEWHLPLNDGNHNRLRDDASLNLRNGITAIWIPPAWKGTSONDVGCGA 60
DB 34 HHNGTNGTMMQYFEWHLPLNDGNHNRLNDSASLNKSGITAVWIPPAWKASQNDVGCGA 93
QY 61 YDLYDLGEFNGKQVTRTKYQTRSQLESIAIHALKNGVQVYGDVVNMHKGADATENVLAV 120
DB 94 YDLYDLGEFNGKQVTRTKYQTRSQQAATVSLKNGGIQVYGDVVNMHKGADATEMVRVAV 153
QY 121 EVNPNRNRQISGDYITTEAWTKDFPGRGNTYSDFKRWVHFDGVQDWDQSRQFNRIYKF 180
DB 154 EVNPNRNRQVTEYITTEAWTRDFDPRGRNTHSFSKRWVHFDGVQDWDQSRRLNRIYKF 213
QY 181 RGDGKAWDWEVDSENGNYDLYMADVDMHPEVVNELRRWGEWYTNLTLDGFRIDAVKH 240
DB 214 RGHGKAWDWEVDTEGNYDLYMADIDMDHPEVVNELRWGVYTNLTGLDGRIDAVKH 273
QY 241 IKYSFTRDWLTHVRNATGKEMPAVAFWPKNDLGALENYLNKTNWNSHVFDPVPLHYNLYNA 300
DB 274 IKYSFTRDWINHVRSATGKNMFAVAFWPKNDLGALENYLNKTNWNSHVFDPVPLHYNLYNA 333
QY 301 SNSGGNYDMAKLTNGTVQHPHATVFDVNDHDSQCESLESFVQEFKPLAYALITRE 360
DB 334 SKSGGNYDMENIFNGTVQHPHSHAVTFVNDHDSQPEALESFVEWFKPLAYALITRE 393
QY 361 QGYPSVFGYDYGIPTHSVPAKAKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRBGNNT 420
DB 394 QGYPSVFGYDYGIPTHGVPAKSKIDPILAEARQNFAYGTQHDYFDHNNIIGWTRBGNNTA 453
QY 421 HPNSGLATIMSDGPGGKMYGVQNKAGQVWHITGNKPTGTVINADGWANFVNGGSVS 480
DB 454 HPNSGLATIMSDGAGGSKMVFGRNKGQVWSDITGNRTGTVINADGWANFVNGGSVS 513
QY 481 IWYKR 485
DB 514 IWVWK 518
RESULT 2
AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (BLA).
GN AMYS OR AMYL.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1] :
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=86111694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amylases
RT deduced from the DNA sequences."
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RL J. Biochem. 98:1147-1156(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=861195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamea M.H., Kindle K.L.,
RA Carmona C., Requadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [3]
RP SEQUENCE FROM N.A.
RA Shahhoseini M., Ziaei A.A., Ghaemi N., Pourbabaee A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RN Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Orlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372(1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Laioide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amylL, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442(1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2192788; PubMed=11997021;
RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltooligosaccharide substrates.";
RL FEBS Lett. 518:79-82(2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RC STRAIN=ATCC 6598; PubMed=2394736;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Gaillardin C., Maeson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
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RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Gaillardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RT modulation of its stability over a 50 degrees C temperature range.";
RN Protein Eng. 16:287-293(2003).
RN [12]
RN RP MUTAGENESIS OF TRP-292 AND VAL-315.
RN STRAIN=ATCC 27811;
RN MEDLINE=22797417; PubMed=12915728;
RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;
RT "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycoylation
RT activity.";
RN Protein Eng. 16:505-514(2003).
RN [13]
RN RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RN STRAIN=ATCC 27811;
RN MEDLINE=95182462; PubMed=787175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RT amylase at 2.2-A resolution.";
RN J. Mol. Biol. 246:545-559(1995).
RN [14]
RN RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RN MEDLINE=98212915; PubMed=9551551;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Activation of Bacillus licheniformis alpha-amylase through a
RT disorder-->order transition of the substrate-binding site mediated
RT by a calcium-sodium-calcium metal triad.";
RN Structure 6:281-292(1998).
RN [15]
RN RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.
RN MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Bauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.
RT High-resolution analysis of native and ligand complexes.";
RN Biochemistry 39:9099-9107(2000).
RN [16]
RN RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
RN HL62V/N219F/A238V/Q293S/N294Y.
RN STRAIN=ATCC 6598;
RN MEDLINE=22538505; PubMed=12540849;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
RT introduction of hydrophobic residues at the surface.";
RN J. Biol. Chem. 278:11546-11553(2003).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
CC liquefaction of starch-containing mashes and in the detergent
CC industry to remove starch. Sold under the name Termamyl by
CC Novozymes.
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
CC values (up to pH 11) and at high temperatures (up to 100 degrees
CC Celsius).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; X03236; CAA26981.1; -
DR EMBL; M38570; AAA22226.1; -
DR EMBL; M13256; AAA22240.1; -
DR EMBL; K01984; AAA22193.1; -

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DR EMBL; AF438149; AAO26743.1; -
DR EMBL; M26412; AAA22337.1; -
DR EMBL; A17930; CAA01355.1; -
DR PIR; A91997; ALES1.
DR PDB; 1BLI; 23-MAR-99.
DR PDB; 1BPL; 17-AUG-96.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR PDB; 1O80; 03-APR-03.
DR PDB; 1VJS; 12-MAR-97.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 512
FT ACT_SITE 260 260
FT ACT_SITE 264 264
FT ACT_SITE 357 357
FT METAL 133 133
FT METAL 190 190
FT METAL 210 210
FT METAL 212 212
FT METAL 223 223
FT METAL 229 229
FT METAL 231 231
FT METAL 233 233
Query Match 71.6%; Score 1947; DB 1; Length 512;
Best Local Similarity 70.4%; Pred. No. 4.3e-124;
Matches 340; Conservative 64; Mismatches 73; Indels 6; Gaps 3;
Qy 6 NGTMMQYFEWHLNDGNHNNRLRDASNLNRRGITAIPPAWKGTSQNDVGVGAYDLYD 65
Db 33 NGTLMQYFEWYMPNDGQHWKRLQND SAYLAELHGTAWIPPAWKGTSQADVGVGAYDLYD 92
Qy 66 LGFBNQKGTVRTYKTRTSQLESIAHAKNNGVOYGVGVVNNHKGADATENVLAVENPN 125
Db 93 LGFHFQKGTVRTYKTKGELQSAIKSLHSRDINVYGDVINHKGADATEDVTAVEVDP 152
Qy 126 NRQETISGDYIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDQSRQFQNRVYKFRGDGK 185
Db 153 DRNRVISGEHRIKAWTHFHPGRGSTYSDFKRWYHFDGVDWDQSRQFQNRVYKFRGDGK 209
Qy 186 ADWEVDSNGNDYLMYADVDMDHPEVNVNLRWGEWYTNLNLGDFRIDAVKHIKYSF 245
Db 210 ADWEVSNNGNDYLMYADVDMDHPEVNVNLRWGEWYTNLNLGDFRIDAVKHIKYSF 269
Qy 246 TRDLWTHVRNATGKEMFVAEAFWKNDLGALENLYNKTNNHNSVDFVPLHYNLNNSGSG 305
Db 270 LRDNVNVHREKTKGEMFVAEAFWKNDLGALENLYNKTNNHNSVDFVPLHYNLNNSGSG 329
Qy 306 NYDMAKLLNGTGVQKHPMHAVTFVDNHDSDQPSLESFVQEWKPKLAYALITREQGPS 365
Db 330 GYDMRKLNLNVTWSKHPKAVTFVDNHDSDQPSLESFVQEWKPKLAYALITREQGPS 389
Qy 366 VFYGVYGIPTHS---VPAMKAKIDPILAEARONFAYGTHDYPDHNNIIGWTRGNTHP 422
Db 390 VFYGVDMGTGKDSQREIPALKHKIEPLKARKKAYGAQHDYFDHHDIVGWTREGDSVA 449
Qy 423 NSGLATTMSDGPGEKWMYVGQNKAGQVHWDITGNKFGTVTINADGWANFVNSGGSYSIW 482
Db 450 NSGLAALITDGPGEKWMYVGQNKAGQVHWDITGNKFGTVTINADGWANFVNSGGSYSIW 509
Qy 483 VKR 485
Db 510 VQR 512

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Db 159 DRNQESGTTQIQAWTKDFPGRNTYSSPKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 AWDEWVDSNGTNDYLMYADVMDHPVAVNELRWGEWYNTNLNDCGFRIDAVKHIXYSF 245
Db 218 AWDEWVDSNGTNDYLMYADVMDHPVAVNELRWGEWYNTNLNDCGFRIDAVKHIXYSF 277
Qy 246 TRDLWTHVRNATGKEMPAFAEFKNDIGALENYLNTKTNHNSVDPVPLHYNLNNSGSG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYNSYDINKLHNYIMKTNGTMSLFPDAPLHNFYTSKSGG 337
Qy 306 NYDMAKLLNTVVQKHPHVAFTVDNHSQGESLESFVQWFKPLAYALILREQQYPS 365
Db 338 TFDMTLMTLTKMOQTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEGYPC 397
Qy 366 VFYGDYGIPTSSVPAMKAKIDPILKARQNFAYGTQHDYFDHNIIGWTREGNTHNSG 425
Db 398 VFYGDYGIPTSSVPAMKAKIDPILKARQNFAYGTQHDYFDHNIIGWTREGNTHNSG 457
Qy 426 LATIMSDGPGGKWMYVQNGKAGQVWHDTITGNKPGTITINADGWANFVNGSGSVIWXR 485
Db 458 LAALITDGPCKWYVQNGKAGQVWHDTITGNKPGTITINADGWANFVNGSGSVIWXR 517

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RESULT 4

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ID AMY_BACAM STANDARD; PRT; 514 AA.
AC P00692;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
RA Kaeaeiaainen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
RT deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RP SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
RT amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
RA Soederlund H., Takkinen K., Kaeaeiaainen L.;
RT Nucleotide sequence of the promoter and NH2-terminal signal peptide
RT region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
RT its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkmenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.

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RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:19099-9107(2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC or send an email to license@isb-sib.ch).
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DR EMBL; J01542; AAA22191.1; -
DR EMBL; V00092; CAA23430.1; -
DR EMBL; A20154; CAA01489.1; -
DR EMBL; M18424; AAA22192.1; -
DR PIR; A92389; ALBSN.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 514 ALPHA-AMYLASE.
FT ACT_SITE 262 262
FT ACT_SITE 292 292
FT ACT_SITE 359 359
FT METAL 133 133
FT METAL 190 190
FT METAL 212 212
FT METAL 214 214
FT METAL 225 225
FT METAL 231 231
FT METAL 233 233
FT METAL 235 235
FT METAL 266 266
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FT METAL 461 461
FT CONFLICT 54 54
FT CONFLICT 64 64
FT CONFLICT 79 79
FT CONFLICT 84 84
FT SEQUENCE 514 AA; 59403 MW; 3DE66B3FB5CCDE7E CRC64;
Query Match 68.8%; Score 1871; DB 1; Length 514;
Best Local Similarity 67.9%; Pred. No. 5,7e-119;
Matches 330; Conservative 65; Mismatches 87; Indels 4; Gaps 2;
Qy 3 NGTGTMMQYFEWHLPNNGHNNRLRDDASLNRRGITAIIWIPPAWKGTSQNDVGYGAYD 62
Db 30 SAVNGTLMQYFEWHTPNDGQHKRLQNDASHLSDIGITAWIIPAYKGLSQNDGYGYD 89
Qy 63 LYDLGEFNQKGTVRTKYGTSTQLESALHAKNNGVQYVGVVMMHKGADATENVLAVEV 122
Db 90 LYDLGEFQKGTVRTKYGTSELQDAIGSLHSRNVQYVGVVNLHKGADATEDVTAVEV 149
Qy 123 NPNNRNQEISGDYTIETAWTKDFPGRNTYSSPKRWYHFDGVDWDSRKL-SRIYKFRG 182
Db 150 NPNNRNQEISGDYTIETAWTKDFPGRNTYSSPKRWYHFDGVDWDSRKL-SRIYKFRG 208

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QY 183 DGKAWDEVDSENGNDYLMYADVDMDPHPVAVNELRRWGEWYNTNLNLDGFRIDAVKHK 242
Db 209 EGRADWEVSENGNDYLMYADVDMDPHPVAVNELRRWGEWYNTNLNLDGFRIDAAKHK 268
QY 243 YSTRWLTHVRNATGKEMFAVAFWKNLIDGALENYLNKTNHNSVDPVPLHYNLYASN 302
Db 269 FSLRDWQVROATGKEMFTVAEYQNNAGKLENYLNKTSFNQSPVDPVPLHFNLOAAS 328
QY 303 SGNGYDMAKLLNGTVVQKHPMHAFTFVDNHDSPGSELESFVQWPKPLAYALILFREOG 362
Db 329 QGGYDMRLLDGTVSRHEKAVFTVENHDTOPGQSELSVTQWPKPLAYAAILFREOG 398
QY 363 YPSVFYDYGIGIPHS---VPAMKAKIDPILARQNFAYGTQHDYFDHNNIIGWTREGNT 419
Db 389 YPQVFYDGMVGTGTPKPSLKNIEPIILKARKEYAVGPQHDYIDHPDVIGWTREGDS 448
QY 420 THPNSGLATIMSOPGGEKWMYQONKAGQVWHDITGNKPGTITINADGWANFSVNGSV 479
Db 449 SAAKSGLAALITDPGSGSKRMYAGLKNAGETWYDITGNRSDTVKIGSDGMGEFHVNDGSV 508
QY 480 SIWVKR 485
Db 509 SIYQK 514

RESULT 5
AMV2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
AT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR STM1963;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=SUW1103;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [3];
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=SUW1103;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [4];
RP SEQUENCE OF 476-494 FROM N.A.
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIb, including a
```

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RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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DR EMBL; L01643; AAA27110.1; -.
DR EMBL; AB008787; AAL20875.1; -.
DR EMBL; M85241; AAA27079.1; -.
DR EMBL; L13280; AAA1970.1; -.
DR PIR; B45738; B45738.
DR KSSP; P06278; 1VJS.
DR StyGene; SG10011; amyA.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5E47C CRC64;
Query Match 39.8%; Score 1082; DB 1; Length 494;
Best Local Similarity 42.5%; Pred. No. 8.1e-66;
Matches 209; Conservative 82; Mismatches 183; Indels 18; Gaps 6;
QY 6 NGTMQYFEWHLFNDGNHNRRLRDDASLNRRNGITAIWIPPAWKGTSON-DVGYGAYDLY 64
Db 3 NPTLLQYFHWYVDPGGKLSLSAERADGLNDGINNWLPPACKGASGGVSGYDYDLY 62
QY 65 DLGEFNQKGTVTIKYTRQSLESAHALKNGVQVYGVDMVHMKGGADATENVLAVSNP 124
Db 63 DLGEFDQKGTIATKYGDKRQLTALDALKKNIAVLDDVNVHMGADAKERIRVORVQ 122
QY 125 NNRNQBISGDYTIAMTKDFPGRGNTYSDFKWRVYHFDGVWDQSRQFNRIYKFRGD- 183
Db 123 DRTQTDNNIIECEGTRTFFPARAGQYGNFWDYHCFSGIDHIEFPD-EDGFKIWDY 181
QY 184 -GKAMDWEVDSENGNDYLMYADVDMDPHPVAVNELRRWGEWYNTNLNLDGFRIDAVKHK 242
Db 182 TGDGWNQDQVDEMGNFDYLMGENIDPRNHAFTVEIKYWARVWMEQTHCDGFRIDAVKHIP 241
QY 243 YSFTRDLWTHVRNATGKEMFAVAFWKNLIDGALENYLNKTNHNSVDPVPLHYNLYASN 302
Db 242 AMFYKEWIEHVQAVAPKPLFIVAEYVSHVDEKLTQYIDQVQDKTMLFDAPLQMKFHEASR 301
QY 303 SGNGYDMAKLLNGTVVQKHPMHAFTFVDNHDSPGSELESFVQWPKPLAYALILFREOG 362
Db 302 QGAEDVMRHI FTGTLVEADPFHAVTLVANHDTPLOALEAPVEPWFKPLAYALILRENG 361
QY 363 YPSVFYDYGIGIPHS-----SVPAMKAKIDPILARQNFAYGTQHDYFDHNNI 411
Db 362 VPSVFYDLYGASYESGSENGETCTCRVDMFVIN-QLDRLILARQRFAGHGTTLFFDHPNCI 420
QY 412 GWTREGNTTHPSGLATIMSOPGGEKWMYQONKAGQVWHDITGNKPGTITINADGWAN 471
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Db 421 AFRSG--TEENPCVVVLNSGDDGKTKLLGDNANYANKTWRDFLGNRDEYVVTNDQGEAT 478

QY 472 FSVNGGVSIVW 483

Db 479 FFCNAGSVSVW 490

RESULT 6

ID AMY2_ECOLI STANDARD; PRT; 495 AA.

AC P26612; P78072;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan

DE glucanohydrolase).

GN AMYA OR B1927.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JAI1;

RX MEDLINE=93015717; PubMed=1400215;

RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;

RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";

RL J. Bacteriol. 174:6644-6652(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MGI655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97251359; PubMed=9097040;

RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,

RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,

RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,

RA Saito N., Sanpei G., Seki Y., Sivasubram S., Tagami H.,

RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;

RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 40.1-50.0 min region on the linkage map.";

RL DNA Res. 3:379-392(1996).

RN [4]

RP SEQUENCE OF 1-5 FROM N.A.

RC STRAIN=JAI1;

RX MEDLINE=92407478; PubMed=1527488;

RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;

RT "Subdivision of the Escherichia coli and Salmonella typhimurium

RT chromosomes between flagellar regions IIIa and IIb, including a

RT large non-coding region.";

RT additional flagellar genes.";

RL J. Gen. Microbiol. 138:1051-1065 (1992).

RN [5]

RP SEQUENCE OF 475-495 FROM N.A.

RC STRAIN=JAI1;

RX MEDLINE=93381452; PubMed=8371104;

RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;

RT "Organization of the Escherichia coli and Salmonella typhimurium

RT chromosomes between flagellar regions IIIa and IIb, including a

RT large non-coding region.";

RL J. Gen. Microbiol. 139:1401-1407(1993).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

CC linkages in oligosaccharides and polysaccharides.

CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

CC -1- SUBUNIT: Monomer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

CC EMBL; L01642; AAA23810.1; -

DR EMBL; AB000285; AAC74994.1; -

DR EMBL; D90833; BAA15755.1; -

DR EMBL; M85240; -; NOT ANNOTATED_CDS.

DR EMBL; L13279; AAA82575.1; -

DR PIR; D64956; A45738.

DR HSP; P06278; 1VJS.

DR EcoGene; EG11387; amyA.

DR InterPro; IPR006589; Alp_amyl_cat_sub.

DR InterPro; IPR006047; Alpha_amyl_cat.

DR Pfam; PF00128; alpha-amylase; 1.

DR SMART; SM00642; Amy; 1.

KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;

KW Complete proteome.

FT ACT_SITE 235 235 BY SIMILARITY.

FT ACT_SITE 265 265 BY SIMILARITY.

FT ACT_SITE 332 332 BY SIMILARITY.

FT METAL 104 104 CALCIUM (BY SIMILARITY).

FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY

FT SIMILARITY).

FT CONFLICT 19 20 KL -> SS (IN REF. 1).

FT CONFLICT 109 109 A -> V (IN REF. 1).

FT CONFLICT 149 149 Q -> E (IN REF. 1).

FT CONFLICT 234 234 L -> I (IN REF. 1).

SQ SEQUENCE 495 AA; 56639 MW; 26AFF6797DDA54D6 CRC64;

Query Match 39.1%; Score 1064; DB 1; Length 495;

Best Local Similarity 41.1%; Pred. No. 1.3e-64;

Matches 206; Conservative 86; Mismatches 182; Indels 18; Gaps 6;

QY 6 NGTMQYFEWHLNDGNHNLRLDDASNLNRGITAIPPAKGTSON-DVUGYGYDLY 64

DB 3 NPTLLQCFHWYPEGGKLPDLAERADGFNDIGINVMVLPYPAKGGSGVSGVSYDLF 62

QY 65 DLGEFNQKGTVRTKYGRSOLSAIHALKONGVQVYGVDMNHKGGADAPENYLAVERN 124

DB 63 DLGEFDQKGSIPKYGDQAQLAALDALKRNDIAVLDDVVNNHMKGADEKAEIRVORNA 122

QY 125 NNRNQISGDYTTIEAWTKDFPGRGNTYSDFKRWYHFDGVWDQSRQFQNRYYKFRGD- 183

DB 123 DDRTOIDEEIIECEGTRTYTPPARAGYSQFIWDFKFCSGIDHINPD-EDGIFKIVNDY 181

QY 184 -GXANDWEVDSENGVDYLMYADVMDHDPVNNELRRWGEWYTNLMDGFRIDAVKHK 242

DB 182 TGEWMDQVDELGNFDYLMGENIDFRNHAFTVEIKYWARVWVMEQTCDCDFRLDAVKHIP 241

QY 243 YSTRDMLTHVRNATKEMFAVAFWKNDIGALENYLNKTNHNSVDFDPLHYNLYNASN 302

DB 242 AWFYKIEWIEHVQVAPKPLFVAVIYWSHEVDKLTQTYIDQVEGKTMFLDAPLQMKFHEASR 301

QY 303 SGGNYDMAKLLNGTVVQKHPMHAFTFVDNHDSDPGESESVQVQWFKPLAYALILTREG 362

DB 302 MGRDYDMTQIFCTGLVEADFFHATLVANHDTPLQALEAPVPEVPFKFLAYALILRENG 361

QY 363 YPSVFGDYNGIETHSV-----PAMKAKIDPILAEARQNFAYGTQHDHFDHNII 411

DB 362 VPSVFPDLYGAHYEDVGGDGYTYPIDMPIIE-QLDELILARQRFAGHVQTLFFDHPNCI 420

QY 412 GWTREGNTHPNGLATINSDGPGKWMYVGONKAGQVWHDTGNKPGVTVINADGAN 471

DB 421 AFRSGTDEFP--GCVVVMSNGDDGKTIHLGSENGYGNKTRWRDFLGNRQERQVTDENGAT 478

QY 472 FSVNGGSVSIWV 483
 Db 479 FFCNGGSVSVWV 490

RESULT 7
 AMYB_PABPO STANDARD; PRT; 1196 AA.
 AC P21543;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Beta/alpha-amylase precursor [Includes: Beta-amylase (EC 3.2.1.2);
 DE Alpha-amylase (EC 3.2.1.1)].
 OS Paenibacillus polymyxa (Bacillus polymyxa).
 OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 NCBI_TaxID=1406;
 RN [1]
 RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=72;
 RX MEDLINE=87165765; PubMed=2435707;
 RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
 RA Tsukagoshi N., Udaoka S.;
 RT "Cloning and nucleotide sequence of the gene coding for enzymatically
 RT active fragments of the Bacillus polymyxa beta-amylase.";
 RL J. Bacteriol. 169:1564-1570(1987).
 RN [2]
 RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=72;
 RX MEDLINE=89123046; PubMed=2464578;
 RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
 RA Tsukagoshi N., Udaoka S.;
 RT "A single gene directs synthesis of a precursor protein with beta-
 RT and alpha-amylase activities in Bacillus polymyxa.";
 RL J. Bacteriol. 171:375-382(1989).
 RN [3]
 RP SEQUENCE OF 1-776 FROM N.A.
 RC STRAIN=ATCC 8523;
 RX MEDLINE=87231094; PubMed=2438660;
 RA Rhodes C., Strasser J., Friedberg F.;
 RT "Sequence of an active fragment of B. polymyxa beta amylase.";
 RL Nucleic Acids Res. 15:3934-3934(1987).
 RN [4]
 RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
 RX MEDLINE=91215008; PubMed=1827035;
 RA Uozumi N., Matsuda T., Tsukagoshi N., Udaoka S.;
 RT "Structural and functional roles of cysteine residues of Bacillus
 RT polymyxa beta-amylase.";
 RL Biochemistry 30:4594-4599(1991).
 CC -!- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
 CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
 CC SECRETION.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
 CC polysaccharides so as to remove successive maltose units from the
 CC non-reducing ends of the chains.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: In the N-terminal section; belongs to family 14 of
 CC glycosyl hydrolases.
 CC -!- SIMILARITY: In the C-terminal section; belongs to family 13 of
 CC glycosyl hydrolases.

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 CC -----
 CC EMBL; M15817; AAA85446.1; --
 CC EMBL; Y00150; CAA68344.1; --

DR PIR; A29130; A29130.
 DR HSSP; P36924; 1B9Z.
 DR InterPro; IPR006589; Alp_amyl_cat sub.
 DR InterPro; IPR006048; Alpha_amyl_C.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR005085; CBM_25.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR001554; Glyco_hydro_14.
 DR Pfam; PF02806; alpha-amylase; 1.
 DR Pfam; PF03423; CBM_25; 2.
 DR Pfam; PF01373; Glyco_hydro_14; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR PRINTS; PR00750; BETAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 DR PROSITE; PS00506; BETA-AMYLASE 1; 1.
 DR PROSITE; PS00679; BETA-AMYLASE 2; 1.
 DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
 KW Polysaccharide degradation; Repeat.
 FT SIGNAL 1 35
 FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
 FT DOMAIN 36 454 BETA-AMYLASE.
 FT REPEAT 455 558
 FT REPEAT 565 668
 FT DOMAIN 669 1196 ALPHA-AMYLASE.
 FT DISULFID 118 126
 FT ACT_SITE 198 198
 FT ACT_SITE 394 394
 FT MUTAGEN 118 118
 FT MUTAGEN 126 126
 FT MUTAGEN 358 358
 FT CONFLICT 1 1
 FT CONFLICT 67 67
 FT CONFLICT 100 100
 FT CONFLICT 154 154
 FT CONFLICT 177 177
 FT CONFLICT 227 228
 FT CONFLICT 330 330
 FT CONFLICT 425 425
 FT CONFLICT 493 493
 FT CONFLICT 532 532
 FT CONFLICT 559 559
 FT CONFLICT 665 665
 FT CONFLICT 681 681
 FT CONFLICT 686 686
 FT CONFLICT 725 728
 FT CONFLICT 736 736
 FT CONFLICT 741 741
 FT CONFLICT 758 758
 SQ SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;

Query Match 12.0%; Score 327; DB 1; Length 1196;
 Best Local Similarity 23.4%; Pred. No. 1.8e-14;
 Matches 121; Conservative 70; Mismatches 192; Indels 134; Gaps 24;

QY 1 HNGTNGTMMQVFWEHLFNDGNHNRNRDASNLNRNGITAIWIPPAWKGTSQNDV-GYG 59
 Db 766 NYGFGNSNNSDQKWH- - - - -GGDFGIIKLDYIKMGFTAIWITPTWQKSEYAYHGVH 821
 QY 60 AYDLVDLGEFNQKGTVRTKYKTRSOLESAIHALKNGVGVYGDVVMNHKGGADATENVLA 119
 Db 822 TYDFY- - - - -AVDGLGTMDKQLQELVRKAHKNIAVMVDVNVNHTG- - - - - 862
 QY 120 VEVNPNNEQISGDYTTTEATWKDF-PCRNTYSDP-KWEYHFDGVDWQSQRFQNR 177
 Db 863 - - - - -DFQPGNGFAKAPFDKADWYHHNGIITDGDVYNSNQ- 897
 QY 178 YKFRGDGKAWDEVDSENGNDYLMYADVMDHPVNVNELRRWGEWYTNLTLDGFRIDA 237
 Db 898 - - - - -WKI--ENG--DVAGLDLNLNHNPATANELKNKWLNETGIDGLRDT 942
 QY 238 VKHIKYSFTRDLWLTNVRNATGKEMFAVAFWKNLDGALENLYLNKTNWNSHVSFDPVPLHNL 297


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FT STRAND 383 387
FT STRAND 393 398
FT STRAND 403 408
FT HELIX 415 417
FT TURN 418 418
FT STRAND 424 429
FT TURN 430 433
FT STRAND 434 438
SQ SEQUENCE 548 AA; 59876 MW; 2B87217B3379158F CRC64;

Query Match 10.1%; Score 275; DB 1; Length 548;
Best Local Similarity 25.5%; Pred. No. 2.3e-11;
Matches 133; Conservative 64; Mismatches 167; Indels 158; Gaps 28;

QY 2 HNGTNGTMMQYFEHML-----PNDGNHNRRLRDDASNLNRGITAITWIPPAWKGTSONDVG 57
DB 33 YHGDEIILQGFHNVVREAPND--WYNILRQQAATTAADGFSALWVPWRDSSWSDG 90
QY 58 --YGAYDLYDLGEPNQKGTVRTKGTROLSAIAHALKNGVQVGVVNMH--KGADA 113
DB 91 SKSGGEGYFHWDFNKG---RYGSDAQLRQAASALGGAGVKLYDVVPHNMRGYEDK 146
QY 114 TENVLAVEVPPNENQIEISDGYTTEATWKDFPCRGNTYSDFKWRWYHFDGVDWDQSRQF 173
DB 147 EINLPAG-----QGFWRNDCADPGN-YFN-----DCDDGDRF 177
QY 174 QNRIYKFRGKAWDEWVDSENGNYDYLMTADVMDHPPEVNNELRRWGEWYTN---TLNL 230
DB 178 -----IGGD-----ADLNTGHPVYGMFR---DEFTNLRSQYGA 208
QY 231 DGFRIADVHIKYSFTRDMLTHVRNATGKEMFAVAEFWKNDLGALE-----NYLNKTNWNH 286
DB 209 GGRFDFVRGYPVRSVNSMTD---SADNSFCVGLWK---GPSEYPNMDWRNTASWQ 261
QY 287 -----SVFDPVLYNLVNASNSGNYDMAKLLNGTVQKHPMHAATFVDNHD- 334
DB 262 IIKWDSRAKCPVDFDFALKERMONGSIA---DWKHLGNPNDRPRWEAVTFVDNHDG 317
QY 335 -----QPESLESFVQEFKPLAYALITREOGYPSVF-----YGDYGIPTHSVPAM 382
DB 318 YSPQNGQGHWAQDGLIRQAYAILT-SFGTPVYVWSHMYDWGYGDF----- 365
QY 383 KAKIDPILAEARONPAYGTQHDYFDHNIIGWTRGNTTHPNSGIATIMSDPGGKRWYV 442
DB 366 ---IRQLIQVR--AAGVRAD-----SAISFHSYSGLVATVSGSQQLLV 406
QY 443 QNKAGQVHDTITGKGTGTVINADGWANFSVN--GGSVSIW 482
DB 407 ALNS-----DL-GN-PCQV---ASGSFSEAVNASNGQVRVW 437

RESULT 10
ID AM3A ORISA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE Glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).

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```

CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
CC EMBL; X56336; CAA39776.1; -.
CC PIR; S14958; S14958.
CC HSP; P04063; IAVA.
CC Gramene; P27932; -.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 440
FT ACT_SITE 207 207 ALPHA-AMYLASE ISOZYME 3A.
FT ACT_SITE 315 315 BY SIMILARITY.
FT METAL 119 119 CALCIUM 1 (BY SIMILARITY).
FT METAL 145 145 CALCIUM 2 (BY SIMILARITY).
FT METAL 155 155 CALCIUM 3 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 3 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 170 170 CALCIUM 1 (BY SIMILARITY).
FT METAL 171 171 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 176 176 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 10.1%; Score 274.5; DB 1; Length 440;
Best Local Similarity 24.4%; Pred. No. 1.9e-11;
Matches 112; Conservative 55; Mismatches 167; Indels 125; Gaps 19;

QY 9 MMQYFEW-HLPNDGNHNRRLRDDASNLNRGITAITWIPPAWKGTSONDVGAYDLYDLG 67
DB 31 LFGFNWDSWKQGGWYMLKQVGDIASAGVTHVLPPTTHSVSPQ--GYMPGLYDLN 88
QY 68 EFNQGTVRTKGTROLSAIAHALKNGVQVGVVNMHKGADATENVLAVEVPPN 127
DB 89 -----ASKYGTGKAEKSLIAFAHAKGKCAVDIVNHRCADD----- 125
QY 128 NOEISGDYTTAEATWKDFPCRGNTYSDFKWRWYHFDGVDWDQSRQFONRIYKFRGDKAW 187
DB 126 -KQGRGVIC-----FKGGPR-----GCLDWGSPMICDDTQYSDGTG--- 163
QY 188 DWEVDSNGNYDYLMTADVMDHPPEVNNELRRWGEWYTNLNLGFRIDAVKHICYFTR 247
DB 164 -----HRDTGADFAAPDIDHNLPLVQRELSDLRLRLRRDVGDFGWLDPKAGYSAVAR 218
QY 248 DMLTHVRNATGKEMFAVAEFWKNDL-----ALENYLNKTNWNHVSFV 291
DB 219 ---TVQNA--RPSFVVAEIV--NSLSYDGDGKPAANQDQGRQELVNVVVKVGGSPATADF 272

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QY 292 PLHYNLNYSNAGGNYDMAKLLNGT---VVQKHPHMAVTFVDNHDSPQGSLESFVQEWFP 348
Db 273 TTGKILQSAVQ---GELWRMRDKDGKAPGMIGWYPEKAVTFVDNHDGTGSTRM-----WP 324
QY 349 KP-----LAYALILITREQYPSVFGYDYGIPHTSVPMKAKIDPILFARQNPAYGTOHD 403
Db 325 FPSDKVILGYAYILT-HPGVPCIFYD-----QVFDWNLKQE 359
QY 404 YFDHNNIGWTRGNTHTPNSGLATIMSDGPGGKMYV 442
Db 360 I-----NALAATKRGINAGSKLRVL-----AAESDMVY 389
RESULT 11
ID AM3D ORYSA STANDARD; PRT; 435 AA.
AC P27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.3 OR AMY3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91082278; PubMed=2263460;
RA Huang N., Koizumi N., Reinl S., Rodriguez R.L.;
RA "Structural organization and differential expression of rice alpha-
RT amylase genes";
RL Nucleic Acids Res. 18:7007-7014(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
RA Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: Characterization of cDNA
RT clones and mRNA expression during seed germination";
RL Mol. Gen. Genet. 221:235-244(1990).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Is expressed in all tissues, except in
CC immature seeds. Is the most abundant alpha-amylase isozyme in
CC callus.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurones cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; M59351; AAA33895.1; -;
DR EMBL; M24287; AAA33886.1; -;
DR PIR; S12625; S12625.
DR HSSP; P04063; IAVA.
DR Gramene; P27933; -;
DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 435 ALPHA-AMYLASE ISOZYME 3D.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 311 311 BY SIMILARITY.
FT METAL 116 116 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 136 136 CALCIUM 2 (BY SIMILARITY).
FT METAL 138 138 CALCIUM 2 (BY SIMILARITY).
FT METAL 141 141 CALCIUM 2 (BY SIMILARITY).
FT METAL 151 151 CALCIUM 3 (BY SIMILARITY).
FT METAL 162 162 CALCIUM 3 (BY SIMILARITY).
FT METAL 167 167 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT METAL 170 170 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT METAL 172 172 CALCIUM 1 AND 3 (BY SIMILARITY).
FT CONFLICT 73 74 PQ -> R (IN REF. 2).
FT CONFLICT 137 137 P -> R (IN REF. 2).
SQ SEQUENCE 435 AA; 47911 MW; 1BBD6AB195BA0D6E CRC64;
Query Match 9.7%; Score 264.5; DB 1; Length 435;
Best Local Similarity 22.5%; Pred. No. 8.8e-11;
Matches 120; Conservative 63; Mismatches 171; Indels 179; Gaps 26;
QY 2 HNGTNGTMMQYFEWH-LPNDGNHNRRLRDDASLNRRGITAIPWPAWKTQNDVGYGA 60
Db 21 NSQQAQLVFGFNWESKQGGWYNMLKGQVDDIAKAGVTHVWLPSPSHVAPQ--GYMP 78
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLESATHALKNNGVQVGVDMNHKGGADATENVLAV 120
Db 79 GRLYDLDD-----ASKYGTAAELKSLTAAFHGKGVQCVADVIVNHRCA----- 120
QY 121 EVNPNRNRQEISGDYVTEAWTKFDPFGRGNTYSDFKRWYHFDGVDW-----DOSRQF 173
Db 121 -----EKDARGVVCV-----FE-----GGTP-----DRLDWGPGMCSDDTQVS 155
QY 174 QNRIYKFRGDGKAWDEVDSENGYDYLMYADVDMDH--PEVYNELRRWGEWYTNLTNLD 231
Db 156 DGTGHRDTGEG-----FGAAPDIDHLNPRVQRELTDLNMLKSDVGF 198
QY 232 GERIDAVKHKYSFTFEDMLTHVRN---ATGKEMFAVAEFPKN-----DLGAL 275
Db 199 GWRLD-----FAKGYSTDIAKMYVESCKPGFVVVAEINWSLSYNGDGKPAANOQGRQ 250
QY 276 E--NYLNTKTNWNSVDFDPLHNLNYSNAGGNYDMAKLLNGT-----VVQKHPHMAVTF 328
Db 251 ELVNVNVAVGGAFTFD-----FTTKLQAGVQGELEWLRDNGKAPGMIGWLPKAVTF 306
QY 329 VDNHDSQPQGESLESFVQEWKPL-AYALILITREQYPSVFGYDYGIPHTSVPMKAKID 387
Db 307 VDNHDTGTSQKLWPPSPD--KVMQGYAYILT-HPGVPCIFY----- 344
QY 388 PILEARQNPAYGTQHDYFDHNNIGWT-----REGNTHTPNSGLATIMSDPG- 435
Db 345 -----DH--MFDWNLKQEIATAAIRENRGINAGSKLRIVVADADAY 384
QY 436 ----GEKMYVYQNKAGQVWHDTITGNKPTVTINADGWANFSVNGSVSIWVK 484
Db 385 VAVVDEKVMV-----KIG-TRYDVGNVPSDF-----HQTVHGKDISVWEK 424
RESULT 12
AMT4_PSESA
ID AMT4_PSESA
AC P22963;
DT 01-AUG-1991 (Rel. 19, Created)


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Db 27 LFCQFNHESWKHNGWYNFLMGKVDYDIAAGITHVWLPASQSAEQ--GYMPCRLYDLD 84
Qy 68 EFNQKGTVRTYKTRQSLESAIHALKNGVQVGVVMMHKGADATENVLAEVNPNNR 127
Db 85 -----ASKYGNKAQLKSLGALHGKGVKAIADIVINHR-----TAE 120
Qy 128 NOEISGDYTTAEAWTKFDFPGRGNTYSDFKRWYHFDG-----VDNQSRQFQNRIFYKFR 181
Db 121 HKDGRGIYCI-----FEGGTPDARLDWGP-----HMC 148
Qy 182 GDGKAWDEVDSENGNDYLMYADVMDHDPVNNELRWGEWYTNLNLGDFRIDAVKHI 241
Db 149 RDRPYADGTCNPPTGADFGAAPDIDHLNLVQKELVNLWKADIGFGWRDFPAKY 208
Qy 242 KYSTROWLTHVRNATGKMPAVAEFW-----KNDLGALENYLNKTNWNSHV----- 288
Db 209 SADVAKIYIDR-----SEPSFAVAEITWTSLAYGDKGPNLQDQHRQELVNWVVKVGKG 263
Qy 289 -----FDVPLHNLVNASGNYDMALLNGT-----VVQKHPHVAITFVDNHDSPGE 338
Db 264 PATTFDFTTK--GILNVAVEGLW-----RLRGTDGKAFQCMIGWPAKAVTFVDNHDGTSQ 318
Qy 339 SLESFVCEWFKPLAYALITREQGVPSVFGYGYGIPTHSVPAKAKIDPILAEARQNFAY 398
Db 319 HMPFPFSDRWQ--CYAILT--HPTGTCIFYDHFDM-----GLKBEIDLVSVR----- 365
Qy 399 GTQHDYFDHNNIGWTRGNTHPNGLATIMSGPGGKMWYQNKAGQV-----WH 452
Db 366 -----TRHG--IHNESKLIQIEADAD-----LYLAEID--GRKIVKLGPY 402
Qy 453 DITGNKGTVTINADGNWANSVNGSGSVIWK 484
Db 403 DVGNLIPGFKVAA-----HGNDYAVWEK 426

RESULT 14
CDGT_BACS8
ID CDGT_BACS8 STANDARD; PRT; 713 AA.
AC P17692;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting
DE amylase).
OS Bacillus sp. (strain B1018).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1417;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
RX MEDLINE=90147765; PubMed=1689153;
RA Itokor P., Tsukagoshi N., Uda S.;
RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
RT Bacillus sp. B1018 and its strong homology to the cyclodextrin
RT glucanotransferase genes.";
RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
CC -!- FUNCTION: This endo-type adsorbable amylase is capable to
CC digest raw starch.
CC -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-galactosidic bond.
CC -!- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.iesb-sib.ch/announce/
CC or send an email to license@iesb-sib.ch).
CC -----
DB EMBL; M33302; AAA22239.1; -.
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DR EMBL; D90112; BAA14140.1; -.
DR PIR; S09196; S09196.
DR HSP; P43379; ICDG.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF001128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW Transferase; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713
FT ACT_SITE 256 256
FT ACT_SITE 284 284
FT ACT_SITE 355 355
FT METAL 54 54
FT METAL 56 56
FT METAL 59 59
FT METAL 60 60
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FT METAL 260 260
SQ SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;

Query Match 9.6%; Score 262; DB 1; Length 713;
Best Local Similarity 21.6%; Pred. No. 2.3e-10;
Matches 112; Conservative 88; Mismatches 183; Indels 136; Gaps 24;

Qy 21 GNHW-----NRLRDDASNLNRGITAIIWIPPAWK-----TSQNDVGYGAYDYLDFGEF 69
Db 78 GGDWQGIINKIND--GYLTGMGVTAIWISQFVENIYSIIYSGVNNYTHGYWARDPKKT 135
Qy 70 NQKGTVRTYKTRQSLESAIHALKNGVQVGVVMMHKGADATENVLAEVNPNNR-- 127
Db 136 N-----PAYGTTADFQNLIAAHAKNKIILIDPAPNHTSPASSDQSPFA-----ENGRLY 185
Qy 128 -NOEISGDYTTAEAWTKFDFPGRGNTYSDFKRWYHFDGVDNDQSRQFQNRIFYKRGDKA 186
Db 186 DNGTLLGGYT-----NDTNLPHHNGTDFS----- 211
Qy 187 WDWEVDSENGNDYLMYADVMDHDPVNE-----LRRGEWYTNLNLGDFRIDAVKH 240
Db 212 -----TTENGIIYKNL-YDLADLNHNSTSDVYLKDAIKMMLD-----LGIDGIRMDAVKH 260
Qy 241 IKYSFTDMLTHVRNATGKMPAVAEFW--KNDLGALENYLNKTNWNSHVFDVPLHYNLY 298
Db 261 MPFGQKSFMAAVNNY--KPVFTFGWFLGVNEVGP--ENHKFANESGMSLLDFFPAQKVR 317
Qy 299 NA--SNSGNGYDMAKLINGTVQKHPM--HAVTFVDNHDSPGESLESFVQSWFKPLAYAL 355
Db 318 QVFPDNTDNMYGLKAMLEGSADYAQVDQVTFIDNHDMERFHASNARRKLEQALAFLL 377
Qy 356 ILTRQEQVPSVFG--DYV-----GIPTHSVFA-----MKAKIDPILAEARQNFAY 399
Db 378 ILAR---VPAIYYTEQYMSGGTDPDNRARIPSPSTSTTAYQVTKLAPLRKSNPAIAYG 434
Qy 400 TQHDYFDHNNIGWTRG-----NTTHPNSGLATIMSGPGGKMWYQNK 446
Db 435 STQERWINNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSDFQGS----- 482
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 15.0278 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-4
Perfect score: 2720
Sequence: 1 HHNGTGTMMQYFEWHLPNDDASNRNRURRDDASNRGTAIWIPPAWKTSQNDVCGA 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2720	100.0	485	2	US-08-446-803-2
2	2720	100.0	485	2	US-08-861-837-2
3	2720	100.0	485	3	US-08-600-656-2
4	2720	100.0	485	3	US-09-170-670-2
5	2720	100.0	485	3	US-09-170-670-8
6	2720	100.0	485	3	US-09-193-068-2
7	2720	100.0	485	3	US-09-193-068-8
8	2720	100.0	485	3	US-09-183-412-2
9	2720	100.0	485	3	US-09-183-412-8
10	2720	100.0	485	3	US-09-264-097-5
11	2720	100.0	485	3	US-09-354-191A-2
12	2720	100.0	485	4	US-09-290-734-2
13	2720	100.0	485	4	US-09-230-734-8
14	2720	100.0	485	4	US-09-381-687-3
15	2720	100.0	485	4	US-09-545-586-2
16	2720	100.0	485	4	US-09-545-586-8
17	2720	100.0	485	4	US-09-769-864-2
18	2720	100.0	485	4	US-09-769-864-8
19	2448	90.0	485	2	US-08-446-803-1
20	2448	90.0	485	2	US-08-861-837-1
21	2448	90.0	485	2	US-08-600-908A-12
22	2448	90.0	485	3	US-08-683-838A-12
23	2448	90.0	485	3	US-08-600-656-1
24	2448	90.0	485	3	US-09-170-670-1
25	2448	90.0	485	3	US-09-170-670-7
26	2448	90.0	485	3	US-09-193-068-1
27	2448	90.0	485	3	US-09-193-068-7

28	2448	90.0	485	3	US-09-183-412-1	Sequence 1, Appli
29	2448	90.0	485	3	US-09-183-412-7	Sequence 7, Appli
30	2448	90.0	485	3	US-09-354-191A-1	Sequence 1, Appli
31	2448	90.0	485	4	US-09-291-023A-19	Sequence 19, Appli
32	2448	90.0	485	4	US-09-290-734-1	Sequence 7, Appli
33	2448	90.0	485	4	US-09-290-734-7	Sequence 7, Appli
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36	2448	90.0	485	4	US-09-545-586-1	Sequence 1, Appli
37	2448	90.0	485	4	US-09-545-586-7	Sequence 7, Appli
38	2448	90.0	485	4	US-09-540-715A-19	Sequence 19, Appli
39	2448	90.0	485	4	US-09-769-864-1	Sequence 1, Appli
40	2448	90.0	485	4	US-09-769-864-7	Sequence 7, Appli
41	2444	89.9	485	3	US-09-264-097-7	Sequence 7, Appli
42	2440	89.7	485	4	US-09-381-023A-18	Sequence 18, Appli
43	2440	89.7	485	4	US-09-381-687-1	Sequence 1, Appli
44	2440	89.7	485	4	US-09-540-715A-18	Sequence 18, Appli
45	2440	89.7	516	4	US-09-986-676A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-446-803-2

; Sequence 2, Application US/08446803

; Patent No. 5824531

; GENERAL INFORMATION:

; APPLICANT: Ottrup, Helle

; APPLICANT: Bisgard-Frantzen, Henrik

; APPLICANT: Ostergaard, Peter Rahbek

; APPLICANT: Rasmussen, Michael Dolberg

; APPLICANT: Van Der Zee, Pia

; TITLE OF INVENTION: Alkaline Bacillus Amylase

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5824531o No. 5824531disk of No. 5824531th America

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/446,803

; APPLICATION NUMBER: US/08/446,803

; FILING DATE: 01-June-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Harrington, James J.

; REGISTRATION NUMBER: 38,711

; REFERENCE/DOCKET NUMBER: 4157.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 867-0123

; TELEFAX: (212) 878-9655

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 485 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-446-803-2

; Query Match 100.0%; Score 2720; DB 2; Length 485;

; Best Local Similarity 100.0%; Pred. No. 2.4e-232;

; Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 HHNGTGTMMQYFEWHLPNDDASNRNRURRDDASNRGTAIWIPPAWKTSQNDVCGA 60

Db 1 HNGTNGTMMQYFEWHLPNDDGNNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGFEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120
Db 61 YDLYDLGFEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120
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Db 121 EVNPNRNQEIISGDYTIETAWTKFDPGRGNTYSDFKRWYHFDGVDMQSQRFQNRYYKF 180
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Db 181 RGDGKAWDEVDSENGNTDYLMYADVMDHPVNMELRWGEWYTNLTNLGDFRIDAVKH 240
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Db 301 SNSGGNYDMAKLINGTVVQKHPMAVTVFVNDHDSQGESLESFVQWFKPLAYALILTRE 360
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Db 361 QGYPSVFYDYYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
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Db 421 HPNSGLATIMSDGPGGKEMVYVQNKAGVQVWHIDITGNKPGTVTINADGMANFVSNGSGVS 480
QY 481 IWVKR 485
Db 481 IWVKR 485

RESULT 2

US-08-861-837-2
; Sequence 2, Application US/08861837
; Patent No. 5856164
; GENERAL INFORMATION:
; APPLICANT: Ottrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 58561640 No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,837
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-861-837-2

Query Match 100.0%; Score 2720; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 2.4e-232;

Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HNGTNGTMMQYFEWHLPNDDGNNHNRRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGFEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120
Db 61 YDLYDLGFEFNQKGTVRTKYGTSQLESALHALKNNGVQYGVVNMHKGADATENVLAV 120
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Db 121 EVNPNRNQEIISGDYTIETAWTKFDPGRGNTYSDFKRWYHFDGVDMQSQRFQNRYYKF 180
QY 181 RGDGKAWDEVDSENGNTDYLMYADVMDHPVNMELRWGEWYTNLTNLGDFRIDAVKH 240
Db 181 RGDGKAWDEVDSENGNTDYLMYADVMDHPVNMELRWGEWYTNLTNLGDFRIDAVKH 240
QY 241 IKYSFTRDLWLTNRNATGKEMFAVAFWKNDLGALENYLNKTNMNSHVSFVQWFKPLAYALILTRE 300
Db 241 IKYSFTRDLWLTNRNATGKEMFAVAFWKNDLGALENYLNKTNMNSHVSFVQWFKPLAYALILTRE 300
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Db 301 SNSGGNYDMAKLINGTVVQKHPMAVTVFVNDHDSQGESLESFVQWFKPLAYALILTRE 360
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Db 361 QGYPSVFYDYYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
QY 421 HPNSGLATIMSDGPGGKEMVYVQNKAGVQVWHIDITGNKPGTVTINADGMANFVSNGSGVS 480
Db 421 HPNSGLATIMSDGPGGKEMVYVQNKAGVQVWHIDITGNKPGTVTINADGMANFVSNGSGVS 480
QY 481 IWVKR 485
Db 481 IWVKR 485

RESULT 3

US-08-600-656-2
; Sequence 2, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/600,656
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-600-656-2

Query Match      100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGEFNGKQVTRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120
Db 61 YDLYDLGEFNGKQVTRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120

Qy 121 EVNPNRNRQISGDYTTIEAWTKDFPGRGNTYSDFKRWYHFDGVDQSRQFQNR1YKF 180
Db 121 EVNPNRNRQISGDYTTIEAWTKDFPGRGNTYSDFKRWYHFDGVDQSRQFQNR1YKF 180

Qy 181 RGDKAWDWEVDSENGNYDLYMADVDMDHPVNVNLRWGEWYTNLNDGFRIDAVKH 240
Db 181 RGDKAWDWEVDSENGNYDLYMADVDMDHPVNVNLRWGEWYTNLNDGFRIDAVKH 240

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Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 4
US-09-170-670-2
; Sequence 2, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; EARLIER FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97

Query Match      100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGEFNGKQVTRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120
Db 61 YDLYDLGEFNGKQVTRTKYGRSQAIAHALKNGVQVYGVVNMHKGADATENVLAV 120

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Db 181 RGDKAWDWEVDSENGNYDLYMADVDMDHPVNVNLRWGEWYTNLNDGFRIDAVKH 240

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Db 241 IKYSFTRDMLTHVRNATGKEMFAVAEPWKNDLGALENLKNKNHNSVDFVPLHYNLYNA 300

Qy 301 SNSGNYDMAKLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEFKPLAYALILITRE 360
Db 301 SNSGNYDMAKLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEFKPLAYALILITRE 360

Qy 361 QGYPSVFGYDYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGYDYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420

Qy 421 HPNSGLATIMSDGPGGKWMYVGQNKAGQVWHDTGNKPGVTINADGWANFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVGQNKAGQVWHDTGNKPGVTINADGWANFSVNGGSVS 480

Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 5
US-09-170-670-8
; Sequence 8, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; EARLIER FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
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; ORGANISM: Bacillus sp.	
US-09-170-670-8	
Query Match	
Best Local Similarity 100.0%; Score 2720; DB 3; Length 485;	
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1 H H N G T G T M M O Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60
Qy	61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V V M N H K G G A D A T E N V L A V 120
Db	61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V V M N H K G G A D A T E N V L A V 120
Qy	121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180
Db	121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180
Qy	181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N L D G F R I D A V K H 240
Db	181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N L D G F R I D A V K H 240
Qy	241 I K Y S F T R D M L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300
Db	241 I K Y S F T R D M L T H V R N A T G K E M F A V A E F W K N D L G A L E N Y L N K T N W N H S V F D V P L H Y N L Y N A 300
Qy	301 S N S G G N Y D M A K L L N G T V V Q K P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360
Db	301 S N S G G N Y D M A K L L N G T V V Q K P M H A V T F V D N H D S Q P G E S L E S F V Q S W F K P L A Y A L I L T R E 360
Qy	361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420
Db	361 Q G Y P S V F Y G D Y G I P T H S V P A M K A K I D P I L E A R Q N F A Y G T Q H D Y F D H N I I G W T R E G N T T 420
Qy	421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G S G S V S 480
Db	421 H P N S G L A T I M S D G P G G E K M Y V Q N K A G Q V W H D I T G N K P G T V T I N A D G W A N F S V N G S G S V S 480
Qy	481 I W V K R 485
Db	481 I W V K R 485
RESULT 7	
US-09-193-068-8	
; Sequence 8, Application US/09193068	
; Patent No. 6197565	
; GENERAL INFORMATION:	
; APPLICANT: Svendsen, Allan	
; APPLICANT: Kjøluff, S ren	
; APPLICANT: Bisgaard-Frantzen, Henrik	
; APPLICANT: Andersen, Carsten	
; TITLE OF INVENTION: -Amylase Variants	
; FILE REFERENCE: 5709.000-US	
; CURRENT APPLICATION NUMBER: US/09/193,068	
; CURRENT FILING DATE: 1998-11-16	
; NUMBER OF SEQ ID NOS: 31	
; SOFTWARE: FastSeq for Windows Version 3.0	
; SEQ ID NO 8	
; LENGTH: 485	
; TYPE: PRT	
; ORGANISM: Bacillus sp.	
US-09-193-068-8	
Query Match	
Best Local Similarity 100.0%; Score 2720; DB 3; Length 485;	
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 H H N G T G T M M O Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60
Db	1 H H N G T G T M M O Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60
Qy	61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V V M N H K G G A D A T E N V L A V 120
Db	61 Y D L Y D L G E F N Q K G T V R T K Y G T R S Q L E S A I H A L K N N G V Q V Y G D V V M N H K G G A D A T E N V L A V 120
Qy	121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180
Db	121 E V N P N R N Q E I S G D Y T I E A W T K F D F P G R G N T Y S D F K R W Y H F D G V D W D Q S R Q F N R I Y K F 180
Qy	181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N L D G F R I D A V K H 240
Db	181 R G D G K A W D E V D S E N G N Y D L M Y A D V D M D H P E V V N E L R R W G E W Y T N T L N L D G F R I D A V K H 240
RESULT 6	
US-09-193-068-2	
; Sequence 2, Application US/09193068	
; Patent No. 6197565	
; GENERAL INFORMATION:	
; APPLICANT: Svendsen, Allan	
; APPLICANT: Kjøluff, S ren	
; APPLICANT: Bisgaard-Frantzen, Henrik	
; APPLICANT: Andersen, Carsten	
; TITLE OF INVENTION: -Amylase Variants	
; FILE REFERENCE: 5709.000-US	
; CURRENT APPLICATION NUMBER: US/09/193,068	
; CURRENT FILING DATE: 1998-11-16	
; NUMBER OF SEQ ID NOS: 31	
; SOFTWARE: FastSeq for Windows Version 3.0	
; SEQ ID NO 2	
; LENGTH: 485	
; TYPE: PRT	
; ORGANISM: Bacillus sp.	
US-09-193-068-2	
Query Match	
Best Local Similarity 100.0%; Score 2720; DB 3; Length 485;	
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 H H N G T G T M M O Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60
Db	1 H H N G T G T M M O Y F E W H L P N D G N H N R L R D D A S N L R N G I T A I W I P P A W K G T S Q N D Y G Y G A 60


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Db 241 IKYSFTRDLTHVRNATGKEMFAVAFWKNLGALENLKNKNWHSVDFVPLHYNLA 300
Qy 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYSFVFGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420
Db 361 QGYSFVFGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 10
US-09-264-097-5
; Sequence 5, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: No. 6287826man, Barrie Edmund
; APPLICANT: Hendriksen, Hanne Vang
; TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
; FILE REFERENCE: 5278.200-US
; CURRENT APPLICATION NUMBER: US/09/264,097
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: PA 0321/98
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 60/079,209
; EARLIER FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-264-097-5

Query Match 100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Qy 61 YLDYDLGEFNQKGTVRTKYTRQSLESAIHALKNNGVQVYGVVNMHKGADATENVLAV 120
Db 61 YLDYDLGEFNQKGTVRTKYTRQSLESAIHALKNNGVQVYGVVNMHKGADATENVLAV 120
Qy 121 EVNPNRNRQIESGDYITIAWTKFDPPGNGTYSDFKRWYTHFDGVWDQSQRFQNR1YKF 180
Db 121 EVNPNRNRQIESGDYITIAWTKFDPPGNGTYSDFKRWYTHFDGVWDQSQRFQNR1YKF 180
Qy 181 RGDGKAWDEVDSENGNYDLYMTADVMDHPPEVNVNLRWGEWYTNLNDGFRIDAVKH 240
Db 181 RGDGKAWDEVDSENGNYDLYMTADVMDHPPEVNVNLRWGEWYTNLNDGFRIDAVKH 240
Qy 241 IKYSFTRDLTHVRNATGKEMFAVAFWKNLGALENLKNKNWHSVDFVPLHYNLA 300
Db 241 IKYSFTRDLTHVRNATGKEMFAVAFWKNLGALENLKNKNWHSVDFVPLHYNLA 300
Qy 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYSFVFGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420
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Db 361 QGYSFVFGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVQNKAGQVWHDDITGNKPGTGTINADGWANFVNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 11
US-09-354-191A-2
; Sequence 2, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Prantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-354-191A-2

Query Match 100.0%; Score 2720; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Qy 61 YLDYDLGEFNQKGTVRTKYTRQSLESAIHALKNNGVQVYGVVNMHKGADATENVLAV 120
Db 61 YLDYDLGEFNQKGTVRTKYTRQSLESAIHALKNNGVQVYGVVNMHKGADATENVLAV 120
Qy 121 EVNPNRNRQIESGDYITIAWTKFDPPGNGTYSDFKRWYTHFDGVWDQSQRFQNR1YKF 180
Db 121 EVNPNRNRQIESGDYITIAWTKFDPPGNGTYSDFKRWYTHFDGVWDQSQRFQNR1YKF 180
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Qy 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300
Qy 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Db 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Qy 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420
Db 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485
RESULT 12
US-09-734-2
; Sequence 2, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-2

Query Match 100.0%; Score 2720; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Qy 61 YDLVDLGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120
Db 61 YDLVDLGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120
Qy 121 EVNPNRNRQEIISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSFQNR1YKF 180
Db 121 EVNPNRNRQEIISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSFQNR1YKF 180
Qy 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300
Qy 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Db 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Qy 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420
Db 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420

Qy 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Db 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Qy 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420
Db 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDTGNKPGTVTINADGWANFVSNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485
RESULT 13
US-09-734-8
; Sequence 8, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-8

Query Match 100.0%; Score 2720; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLNDGNHNRRLDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Qy 61 YDLVDLGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120
Db 61 YDLVDLGEFNGKGTVRTKYGTRSQLESIAHALKNGVQVYGDVVMNHKGGADATENVLAV 120
Qy 121 EVNPNRNRQEIISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSFQNR1YKF 180
Db 121 EVNPNRNRQEIISGDYTTIEAWTKFDPGCRGNTYSDFKRWYHFDGVDMDQSFQNR1YKF 180
Qy 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDGKAWDEVDSENGNYDYLMDVDMHDPVNVNLRWGEWYTNLTLDGFRIDAVKH 240
Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVFDVPLHYNLYNA 300
Qy 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Db 301 SNSGNDYDMAKLNGTVVQKHPMAHTFVDNHDSDQGESLESFVQEFKPLAYALILTRE 360
Qy 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420
Db 361 QGYPSVFYDGYGIPHTSVPAKAKIDPILLEARQNFAYGTOHDYFDHNNIIGWTRGNNTT 420

QY 421 HPNSGLATIMSDGPGGKWMYVGONKAGOVVHDIITGNKPGTGTINADGWANFVNGGSVS 480
Db |||||||
QY 421 HPNSGLATIMSDGPGGKWMYVGONKAGOVVHDIITGNKPGTGTINADGWANFVNGGSVS 480
Db |||||||
QY 481 IWVKR 485
Db |||||||
QY 481 IWVKR 485

RESULT 14
US-09-381-687-3
; Sequence 3, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-381-687-3

Query Match 100.0%; Score 2720; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60
Db |||||||
QY 61 YDLYDLGEPNKGTVRTKYTRSQLESIAIHALKNNGVQVYGVVNMHKGADATENVLAV 120
Db |||||||
QY 61 YDLYDLGEPNKGTVRTKYTRSQLESIAIHALKNNGVQVYGVVNMHKGADATENVLAV 120
Db |||||||
QY 121 EVNPNRNQIISGDYTTIEAWTKDFPGRGNTYSDFKRWYHFDGVDQSQRFQNRYYKF 180
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QY 121 EVNPNRNQIISGDYTTIEAWTKDFPGRGNTYSDFKRWYHFDGVDQSQRFQNRYYKF 180
Db |||||||
QY 181 RGDGKAWDWEVDSENGNYDLYMADVMDHPVNNELRRWGEWYTNLNLGDFRIDAVKH 240
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QY 181 RGDGKAWDWEVDSENGNYDLYMADVMDHPVNNELRRWGEWYTNLNLGDFRIDAVKH 240
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QY 241 IKYSFTRDLWTHVRNATGKEMPAFAEFWKNDLGALENYLNKTNMNHVSFVDPVPLHYNLYNA 300
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QY 361 QGYPSVFYGDYIGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTREGNTT 420
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Search completed: October 7, 2004, 00:47:06
Job time : 16.0278 secs

RESULT 15
US-09-545-586-2
; Sequence 2, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchart, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545,586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-2

Query Match 100.0%; Score 2720; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.4e-232;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 RGDGKAWDWEVDSENGNYDLYMADVMDHPVNNELRRWGEWYTNLNLGDFRIDAVKH 240
Db |||||||
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Db |||||||
QY 241 IKYSFTRDLWTHVRNATGKEMPAFAEFWKNDLGALENYLNKTNMNHVSFVDPVPLHYNLYNA 300
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QY 421 HPNSGLATIMSDGPGGKWMYVGONKAGOVVHDIITGNKPGTGTINADGWANFVNGGSVS 480
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Db |||||||
QY 481 IWVKR 485
Db |||||||
QY 481 IWVKR 485

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-4
Perfect score: 2720
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Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2720	100.0	485	9	US-09-769-864-2 Sequence 2, Appli
2	2720	100.0	485	9	US-09-769-864-8 Sequence 8, Appli
3	2720	100.0	485	9	US-09-854-346-4 Sequence 4, Appli
4	2720	100.0	485	9	US-09-902-188A-2 Sequence 2, Appli
5	2720	100.0	485	9	US-09-918-543-4 Sequence 4, Appli
6	2720	100.0	485	9	US-09-795-211-2 Sequence 2, Appli
7	2720	100.0	485	10	US-09-925-576C-4 Sequence 4, Appli
8	2720	100.0	485	12	US-10-665-667-8 Sequence 8, Appli
9	2720	100.0	485	12	US-10-665-667-2 Sequence 2, Appli
10	2720	100.0	485	12	US-10-327-837-2 Sequence 2, Appli
11	2720	100.0	485	12	US-10-327-837-7 Sequence 8, Appli
12	2720	100.0	485	12	US-10-327-837-8 Sequence 4, Appli
13	2720	100.0	485	16	US-10-477-725-4 Sequence 1, Appli
14	2448	90.0	485	9	US-09-769-864-1 Sequence 7, Appli
15	2448	90.0	485	9	US-09-769-864-7 Sequence 7, Appli

16	2448	90.0	485	9	US-09-854-346-2	Sequence 2, Appli
17	2448	90.0	485	9	US-09-902-188A-1	Sequence 1, Appli
18	2448	90.0	485	9	US-09-918-543-2	Sequence 2, Appli
19	2448	90.0	485	9	US-09-795-211-1	Sequence 1, Appli
20	2448	90.0	485	10	US-09-925-576C-2	Sequence 2, Appli
21	2448	90.0	485	12	US-10-665-667-1	Sequence 1, Appli
22	2448	90.0	485	12	US-10-665-667-7	Sequence 7, Appli
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24	2448	90.0	485	12	US-10-327-837-1	Sequence 7, Appli
25	2448	90.0	485	12	US-10-327-837-7	Sequence 12, Appli
26	2448	90.0	485	14	US-10-184-771-12	Sequence 2, Appli
27	2448	90.0	485	16	US-10-477-725-2	Sequence 2, Appli
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29	2440	89.7	516	9	US-09-971-611-2	Sequence 8, Appli
30	2440	89.7	516	16	US-10-399-161-8	Sequence 12, Appli
31	2437	89.6	485	9	US-09-854-346-12	Sequence 12, Appli
32	2437	89.6	485	9	US-09-918-543-12	Sequence 12, Appli
33	2437	89.6	485	10	US-09-925-576C-12	Sequence 24, Appli
34	2437	89.6	485	12	US-10-327-837-24	Sequence 26, Appli
35	2437	89.6	485	12	US-10-327-837-26	Sequence 5, Appli
36	2437	89.6	485	14	US-10-209-812-5	Sequence 12, Appli
37	2437	89.6	485	16	US-10-477-725-12	Sequence 2, Appli
38	2430	89.3	516	16	US-10-343-212-2	Sequence 6, Appli
39	2414	88.8	485	9	US-09-769-864-6	Sequence 13, Appli
40	2414	88.8	485	9	US-09-854-346-13	Sequence 7, Appli
41	2414	88.8	485	9	US-09-902-188A-7	Sequence 6, Appli
42	2414	88.8	485	10	US-09-925-576C-13	Sequence 7, Appli
43	2414	88.8	485	12	US-10-665-667-6	Sequence 6, Appli
44	2414	88.8	485	12	US-10-025-648-7	Sequence 7, Appli
45	2414	88.8	485	12	US-10-327-837-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-769-864-2
; Sequence 2, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-2

Query Match	100.0%	Score 2720;	DB 9;	Length 485;
Best Local Similarity	100.0%;	Pred. No. 1.4e-243;		
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Qy	61	YDLVDLGEFNGKQVTRTKYGTTRSQLESIAIHALKNGVQVGVGVVNMHKGADATENVLAV	120	
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Db 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSDQGESLESFVQEWFKPLAYALLITRE 360
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Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDIITGNKPGTGTVTINADGWANFVNGSGVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 2

US-09-769-864-8
; Sequence 8, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben I.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769, 864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-8

Query Match 100.0%; Score 2720; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRGITAIWIPPAWKGTSONDVGYGA 60
Db 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRGITAIWIPPAWKGTSONDVGYGA 60
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Db 61 YDLIDLGEFQKGTVRTKYTRQSLESIAHALKNNGVQYVGVVNMHKGADATENVLAV 120
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RESULT 3

US-09-854-346-4
; Sequence 4, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-854-346-4

Query Match 100.0%; Score 2720; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLRDDASNLNRGITAIWIPPAWKGTSONDVGYGA 60
Qy 61 YDLIDLGEFQKGTVRTKYTRQSLESIAHALKNNGVQYVGVVNMHKGADATENVLAV 120
Db 61 YDLIDLGEFQKGTVRTKYTRQSLESIAHALKNNGVQYVGVVNMHKGADATENVLAV 120
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Db 181 RGDGKAWDEVDSENGNDYLYMADVMDHPEVNVNLRWGWYTNLTLDGFRIDAVKH 240
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QY 481 IWVKR 485
Db |||||
US-09-795-211-2
RESULT 6
US-09-795-211-2
; Sequence 2, Application US/09795211
; Publication No. US2002018226A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Kasturi, Chandrika
; APPLICANT: Wandstrat, Mark E.
; APPLICANT: Song, Brian X.
; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZY
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: Detergent Composition
; CURRENT APPLICATION NUMBER: US/09/795,211
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: alakaliphilic bacillus
US-09-795-211-2
Query Match 100.0%; Score 2720; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWHL PNDGNHNRRLRDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60
Db |||||
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120
Db YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120
QY 121 EVNPNRNQIEISGDYITIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDQSRQFNRIYKF 180
Db |||||
QY 181 RGDKAWDEVDSENGNYDLYMADVMDHPVNVNLRWGEWYTNLNDGFRIDAVKH 240
Db |||||
QY 241 IKYSFTRDWLTHVRNATGKEMFAVEAFWKNDLGALENLYNKTNNHNSVDFVPLHYNLYNA 300
Db |||||
QY 301 SNSGGNYDMAKLLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
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QY 361 QGYPSVFYGDYVYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420
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QY 481 IWVKR 485

Db 481 IWVKR 485
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RESULT 7
US-09-925-576C-4
; Sequence 4, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-925-576C-4
Query Match 100.0%; Score 2720; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWHL PNDGNHNRRLRDDASNLNRNGITAIWIPPAWKTSQNDVGYGA 60
Db |||||
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120
Db YDLYDLGEFNQKGTVRTKYGTRSQLESIAHALKNNGVQVYGVVNMHKGADATENVLAV 120
QY 121 EVNPNRNQIEISGDYITIEAWTKFDPGRGNTYSDFKRWYHFDGVDWDQSRQFNRIYKF 180
Db |||||
QY 181 RGDKAWDEVDSENGNYDLYMADVMDHPVNVNLRWGEWYTNLNDGFRIDAVKH 240
Db |||||
QY 241 IKYSFTRDWLTHVRNATGKEMFAVEAFWKNDLGALENLYNKTNNHNSVDFVPLHYNLYNA 300
Db |||||
QY 301 SNSGGNYDMAKLLNGTVVQKHPMAHTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db |||||
QY 361 QGYPSVFYGDYVYGIPTHSVPAMKAKIDPILFARQNFAYGTQHDYFDHNIIGWTREGNTT 420
Db |||||
QY 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDDITGNKPGTGTINADGWANFSVNGGSVS 480
Db |||||
QY 481 IWVKR 485
Db |||||
RESULT 8
US-10-665-667-2
; Sequence 2, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten

```
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-2

Query Match      100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWHLPNNDGNHWNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Db 1 HHNGTNGTMMQYFEWHLPNNDGNHWNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Qy 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKNGGVQVYGDVVMNHKGGADATENVLAV 120
Db 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKNGGVQVYGDVVMNHKGGADATENVLAV 120
Qy 121 EVNPNNRNQEISGDYTTIEAWTKFDFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Db 121 EVNPNNRNQEISGDYTTIEAWTKFDFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Qy 181 RGDKAWDEWDSNGNYDLYMADVDMDHPEVNNELRRGWYNTNLNDGFRIDAVKH 240
Db 181 RGDKAWDEWDSNGNYDLYMADVDMDHPEVNNELRRGWYNTNLNDGFRIDAVKH 240
Qy 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHNSVDFVPLHYNLYNA 300
Qy 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILAEARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILAEARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGTVTINADGWANFVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGTVTINADGWANFVNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 9
US-10-665-667-8
; Sequence 8, Application US/10665667
; Publication No. US20040039368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US

; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-8

Query Match      100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWHLPNNDGNHWNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Db 1 HHNGTNGTMMQYFEWHLPNNDGNHWNRLRDDASNLNRGITAIIWIPPAWKTSQNDVGYGA 60
Qy 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKNGGVQVYGDVVMNHKGGADATENVLAV 120
Db 61 YDLYDLGEFNGKQTVRTKYGTRSOLESAIHALKNGGVQVYGDVVMNHKGGADATENVLAV 120
Qy 121 EVNPNNRNQEISGDYTTIEAWTKFDFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Db 121 EVNPNNRNQEISGDYTTIEAWTKFDFPGRGNTYSDFKWRWYHFDGVDWDQSRQFNRIYKF 180
Qy 181 RGDKAWDEWDSNGNYDLYMADVDMDHPEVNNELRRGWYNTNLNDGFRIDAVKH 240
Db 181 RGDKAWDEWDSNGNYDLYMADVDMDHPEVNNELRRGWYNTNLNDGFRIDAVKH 240
Qy 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTFDLWTHVRNATGKEMFAVAEFKNDLGALENLYNKTNNHNSVDFVPLHYNLYNA 300
Qy 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSGGNYDMAKLLNGTVVQKHPHVAFTVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Qy 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILAEARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGYGYGIPTHSVPAKAKIDPILAEARONFAYGTHQHDYFDHNNIIGWTREGNTT 420
Qy 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGTVTINADGWANFVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKMWYVGNKAGQVWHDITGNKPGTVTINADGWANFVNGGSVS 480
Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 10
US-10-025-648-2
; Sequence 2, Application US/10025648
; Publication No. US20030064908A1
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Novo Nordisk of North America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
```

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/025,648
;; FILING DATE: 19-Dec-2001
;; CLASSIFICATION: <Unknown>
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/600,656
;; FILING DATE: 13-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lambiris, Elias J.
;; REGISTRATION NUMBER: 33,728
;; REFERENCE/DOCKET NUMBER: 4318.204-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 867 0123
;; TELEFAX: 212 867 0298
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 485 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-025-648-2

Query Match 100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60

QY 61 YDLYDLGEFNGKGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120
DB 61 YDLYDLGEFNGKGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120

QY 121 EVNPNNRNQISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHPDGVWDQSQRFQNRIFYK 180
DB 121 EVNPNNRNQISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHPDGVWDQSQRFQNRIFYK 180

QY 181 RGDKAWDEVDSENGNYDYLAVDMDHPEVNNELRRGGEWYTTNLDGFRIDAVKH 240
DB 181 RGDKAWDEVDSENGNYDYLAVDMDHPEVNNELRRGGEWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300

QY 301 SNSGGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360
DB 301 SNSGGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360

QY 361 QGYPSPFYGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420
DB 361 QGYPSPFYGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420

QY 421 HPNSGLATIMSDGPGGKEMVYQNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGKEMVYQNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480

QY 481 IWVKR 485
DB 481 IWVKR 485

RESULT 11
US-10-327-837-2
; Sequence 2, Application US/10327837
; Publication No. US20030211958A1

;; GENERAL INFORMATION:
;; APPLICANT: Svendsen, Allan
;; APPLICANT: Borchert, Torben Vedel
;; APPLICANT: Bisgard-Frantzen Henrik
;; APPLICANT: Outtrup, Helle
;; APPLICANT: Nielsen, Bjarne Ronfeldt
;; APPLICANT: Nielsen, Vibeke Skovgaard
;; APPLICANT: Hoeck, Lisbeth Hedegaard
;; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
;; FILE REFERENCE: 5276.400-US
;; CURRENT APPLICATION NUMBER: US/10/327,837
;; CURRENT FILING DATE: 2002-12-23
;; PRIOR APPLICATION NUMBER: US/09/290,734
;; PRIOR FILING DATE: 1999-04-13
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 485
;; TYPE: PRT
;; ORGANISM: Bacillus sp.
US-10-327-837-2

Query Match 100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60
DB 1 HHNGTGTMMQYFEWHLPNNGNHNRLRDDASNLNRGITAIIWIPPAWKGTSONDVGYGA 60

QY 61 YDLYDLGEFNGKGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120
DB 61 YDLYDLGEFNGKGTVRTKYGTRSQLESIAHALKKNNGVQVYGDVVMNHKGGADATENVLAV 120

QY 121 EVNPNNRNQISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHPDGVWDQSQRFQNRIFYK 180
DB 121 EVNPNNRNQISGDYTTIEAWTKFDFPGRGNTYSDFKRWYHPDGVWDQSQRFQNRIFYK 180

QY 181 RGDKAWDEVDSENGNYDYLAVDMDHPEVNNELRRGGEWYTTNLDGFRIDAVKH 240
DB 181 RGDKAWDEVDSENGNYDYLAVDMDHPEVNNELRRGGEWYTTNLDGFRIDAVKH 240

QY 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300
DB 241 IKYSFTRDMLTHVRNATGKEMFAVAFWKNDLGALENLYNKTNNHNSVFDVPLHYNLYNA 300

QY 301 SNSGGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360
DB 301 SNSGGNYDMAKLLNGTVVQKHPMAVTFVDNHDSPQGESLESFVQSWFKPLAYALILTRE 360

QY 361 QGYPSPFYGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420
DB 361 QGYPSPFYGDYGYGIPTHSVPAKAKIDPILFARQNFAYGTQHDYFDHNNIIGWTRGNTT 420

QY 421 HPNSGLATIMSDGPGGKEMVYQNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480
DB 421 HPNSGLATIMSDGPGGKEMVYQNKAGQVWHDTGNKPGTGTINADGWANFSVNGGSVS 480

QY 481 IWVKR 485
DB 481 IWVKR 485

RESULT 12
US-10-327-837-8
; Sequence 8, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt

; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-10-327-837-8

Query Match 100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGEFQKQGTVRTKYGTRSQLESIAHALKKNQGVQYGVGVVNMHKGADATENVLAV 120
Db 61 YDLYDLGEFQKQGTVRTKYGTRSQLESIAHALKKNQGVQYGVGVVNMHKGADATENVLAV 120

Qy 121 EVNPNRNRQETSGDYTTIEAWTKFDPGRGNTYSDFKRWVHFDGVDQSQRFQNRYYKF 180
Db 121 EVNPNRNRQETSGDYTTIEAWTKFDPGRGNTYSDFKRWVHFDGVDQSQRFQNRYYKF 180

Qy 181 RGDCKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDCKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240

Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300

Qy 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360

Qy 361 QGYPSVFGDYGYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGDYGYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420

Qy 421 HPNSGLATIMSDGPGGKWMYVGONKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVGONKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480

Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 13
US-10-477-725-4
; Sequence 4, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2

Query Match 100.0%; Score 2720; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGEFQKQGTVRTKYGTRSQLESIAHALKKNQGVQYGVGVVNMHKGADATENVLAV 120
Db 61 YDLYDLGEFQKQGTVRTKYGTRSQLESIAHALKKNQGVQYGVGVVNMHKGADATENVLAV 120

Qy 121 EVNPNRNRQETSGDYTTIEAWTKFDPGRGNTYSDFKRWVHFDGVDQSQRFQNRYYKF 180
Db 121 EVNPNRNRQETSGDYTTIEAWTKFDPGRGNTYSDFKRWVHFDGVDQSQRFQNRYYKF 180

Qy 181 RGDCKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDCKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240

Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300

Qy 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360

Qy 361 QGYPSVFGDYGYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGDYGYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420

Qy 421 HPNSGLATIMSDGPGGKWMYVGONKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVGONKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480

Qy 481 IWVKR 485
Db 481 IWVKR 485

Query Match 90.0%; Score 2448; DB 9; Length 485;

; SEQ ID NO 4
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
; US-10-477-725-4

Query Match 100.0%; Score 2720; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.4e-243;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLNDGNHNRRLRDDASNLNRNGITAIWIIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGEFQKQGTVRTKYGTRSQLESIAHALKKNQGVQYGVGVVNMHKGADATENVLAV 120
Db 61 YDLYDLGEFQKQGTVRTKYGTRSQLESIAHALKKNQGVQYGVGVVNMHKGADATENVLAV 120

Qy 121 EVNPNRNRQETSGDYTTIEAWTKFDPGRGNTYSDFKRWVHFDGVDQSQRFQNRYYKF 180
Db 121 EVNPNRNRQETSGDYTTIEAWTKFDPGRGNTYSDFKRWVHFDGVDQSQRFQNRYYKF 180

Qy 181 RGDCKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240
Db 181 RGDCKANDWEVDSNGNYDYLMYADVMDHDPVNVNLRNGEWYTNLTLDGFRIDAVKH 240

Qy 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWNHVSFVDFPLHYNLYNA 300

Qy 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360
Db 301 SNSCGNYDMAKLTNGTVVQKHPMAVTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE 360

Qy 361 QGYPSVFGDYGYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGDYGYGTPHSPVPAKAKIDPILFARQNFAYGTOHDYFDHNNIIGWTREGNTT 420

Qy 421 HPNSGLATIMSDGPGGKWMYVGONKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVGONKAGQVWHDDITGNKPGTVTINADGWANFSVNGGSVS 480

Qy 481 IWVKR 485
Db 481 IWVKR 485

RESULT 14
US-09-769-864-1
; Sequence 1, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
; US-09-769-864-1

Query Match 90.0%; Score 2448; DB 9; Length 485;


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Best Local Similarity 87.2%; Pred. No. 2.5e-218;
Matches 423; Conservative 36; Mismatches 26; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWHLFNDGNGHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMMQYFEWHLFNDGNGHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60

Qy 61 YDLYDLGFEFNQKGTVRTKYGTRNQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIYNAV 120
Db 61 YDLYDLGFEFNQKGTVRTKYGTRNQLQAAVTSLKNGGIQVYGDVVMNHKGGADGTEIYNAV 120

Qy 121 EVNPNRNOEISGDIYIEAWTKFDPGRGNTYSDPKRWYHFDGVDWQSRQFQNRYYKF 180
Db 121 EVNPNRNOEISGDIYIEAWTKFDPGRGNTYSDPKRWYHFDGVDWQSRQFQNRYYKF 180

Qy 181 RGDGKAWDEVDSENGNYDYLMTADVMDHDPVENVNLRWGEWYTNLTLDGPRIDAVKH 240
Db 181 RGDGKAWDEVDSENGNYDYLMTADVMDHDPVENVNLRWGEWYTNLTLDGPRIDAVKH 240

Qy 241 IKYSFTRDMLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDMLTHVRNATGKEMFAVAEFWKNDLGALENYLNKTNWHSVDFVPLHYNLYNA 300

Qy 301 SNSGGYDMRNLNGSVVQKHPHATFVDNHDSPQGESLESFVQWFKPLAYALVLTRE 360
Db 301 SNSGGYDMRNLNGSVVQKHPHATFVDNHDSPQGESLESFVQWFKPLAYALVLTRE 360

Qy 361 QGYPSVFGDYGIPTHSVPAMKAKIDPILFARONFAYGTQHDYFDHNNIIGWTREGNTT 420
Db 361 QGYPSVFGDYGIPTHSVPAMKAKIDPILFARONFAYGTQHDYFDHNNIIGWTREGNTT 420

Qy 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDITGNKPGTGTITINADGMANFVNGGSVS 480
Db 421 HPNSGLATIMSDGPGGKWMYVGNKAGQVWHDITGNKPGTGTITINADGMANFVNGGSVS 480

Qy 481 IWVKR 485
Db 481 VWYKQ 485

Search completed: October 7, 2004, 00:57:26
Job time : 55.4478 secs
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RESULT 15
US-09-769-864-7
; Sequence 7, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-7

Query Match 90.0%; Score 2448; DB 9; Length 485;
Best Local Similarity 87.2%; Pred. No. 2.5e-218;
Matches 423; Conservative 36; Mismatches 26; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMMQYFEWHLFNDGNGHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTNGTMMQYFEWHLFNDGNGHNRLRDDASNLNRNGITAIWIPPAWKGTSONDVGYGA 60
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 62.1733 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-6

Perfect score: 2854

Sequence: 1 AAFNCTMQYFWYLPDDG.....TRPTGEFVRWTEPRLVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2854	100.0	515	2	AAR72449 Bacillus
2	2854	100.0	515	2	AAW31406 Bacillus
3	2854	100.0	515	3	AAV99770 Bacillus
4	2854	100.0	515	4	AAV97547 B. stearo
5	2854	100.0	515	5	ABb06935 B. stearo
6	2854	100.0	515	5	AAU12151 Bacillus
7	2854	100.0	515	5	AAb47852 Bacillus
8	2854	100.0	515	5	ABb76588 Termany1-
9	2847	99.8	514	2	AAV78269 Bacillus
10	2836	99.4	549	6	ABU03090 Alpha amy
11	2832	99.2	549	6	ABU03084 Alpha amy
12	2808	98.4	549	1	AAV70338 Alpha-amy
13	2787	97.7	515	2	AAW31502 Bacillus
14	2787	97.7	515	2	AAW48263 Bacillus
15	2787	97.7	515	2	AAV25153 Bacillus
16	2787	97.7	515	6	ABb99483 Amino aci
17	2783	97.5	559	1	AAV70580 Plasmid p
18	2780	97.4	514	2	AAW12955 Alpha-amy
19	2780	97.4	514	2	AAV15417 Bacillus
20	2780	97.4	514	2	AAV07383 Wild type
21	2780	97.4	514	3	AAV99604 Bacillus
22	2777	97.3	514	3	AAV07389 Mutant Te
23	2776	97.3	572	1	AAV70579 Plasmid p
24	2750	96.4	512	2	AAV07388 Mutant Te
25	2727.5	95.6	548	2	AAW39744 B. stearo

26	2727.5	95.6	548	2	AAV01585	AY01585 An alpha-
27	2727.5	95.6	548	4	AAV65879	AY65879 B. stearo
28	2456	86.1	550	6	ABU03091	ABU03091 Alpha amy
29	2434	85.3	515	1	AAV80575	AAV80575 Mutated a
30	2426	85.0	472	6	ABG70532	ABG70532 Alpha amy
31	2426	85.0	472	6	ABU03082	ABU03082 Alpha amy
32	2414	84.6	546	6	ABU03105	ABU03105 Alpha amy
33	2410	84.4	615	6	ABU03102	ABU03102 Alpha amy
34	2410	84.4	644	6	ABU03106	ABU03106 Alpha amy
35	2402	84.2	564	6	ABU03098	ABU03098 Alpha amy
36	1921	67.3	519	4	AAE09762	AAE09762 Bacillus
37	1921	67.3	519	4	AAE09763	AAE09763 Bacillus
38	1918.5	67.2	485	2	AAW12110	AAW12110 Alpha-amy
39	1917	67.2	519	4	AAE09764	AAE09764 Bacillus
40	1915.5	67.1	485	3	AAE29367	AAE29367 Bacillus
41	1915.5	67.1	485	3	AAV29311	AAV29311 Bacillus
42	1914.5	67.1	485	2	AAW12131	AAW12131 Alpha-amy
43	1913.5	67.0	485	3	AAV29364	AAV29364 Bacillus
44	1913.5	67.0	485	3	AAV29391	AAV29391 Bacillus
45	1912.5	67.0	485	2	AAW12117	AAW12117 Alpha-amy

ALIGNMENTS

RESULT 1

AAV72449

ID AAR72449 standard; protein; 515 AA.

XX AAR72449;

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 01-DEC-1995 (first entry)

XX Bacillus stearothermophilus alpha amylase (mature protein).

XX Alpha amylase; variant; enzyme; detergent; additive; dishwashing;

KW washing; Bacillus licheniformis; Bacillus amyloliquefaciens;

KW Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;

KW thermostable.

XX Geobacillus stearothermophilus.

XX WO9510603-A1.

XX 20-APR-1995.

XX 05-OCT-1994; 94WO-DK000370.

XX 08-OCT-1993; 93DK-00001133.

XX 02-FEB-1994; 94DK-00000140.

XX (NOVO) NOVO-NORDISK AS.

XX Borchert TV, Bisgard-Frantzen H, Svendsen A, Theillers M;

XX Van Der Zee P;

XX WPI; 1995-161790/21.

XX N-PSDB; AAQ88068.

XX New Bacillus derived alpha-amylase variants - having amino acid

XX modifications to improve washing and/or dishwashing performance.

XX Claim 34; Page 11-12; 105pp; English.

XX Variant alpha amylase enzymes which have improved washing and/or as

XX detergent additives. The enzymes have one or more amino acid residues

XX added, deleted or substituted. The variants can also be used for textile

XX desizing prior to scouring, bleaching and dyeing. The variants have

XX improved thermostability, acid/alkaline stability; low temperature

XX optimum; pH optimum; higher hydrolysis velocity and improved tolerance to

XX other composition constituents, e.g. oxidation agents. (Updated on 25-MAR

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CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
CC (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 515 AA;

Query Match      100.0%; Score 2854; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANNLSLIGITALWLPAYKGTSRSDVG YVY 60
Db 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANNLSLIGITALWLPAYKGTSRSDVG YVY 60

QY 61 DLYDLGEFNQKGTVRTKYGTKAQYLOAQIAAHAAGM QYVADVDFDHKGADGTEWDAVE 120
Db 61 DLYDLGEFNQKGTVRTKYGTKAQYLOAQIAAHAAGM QYVADVDFDHKGADGTEWDAVE 120

QY 121 VNPSDRNQEISGTQYIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
Db 121 VNPSDRNQEISGTQYIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180

QY 181 IGKAWDWEVDTEGNYDYLMYADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240
Db 181 IGKAWDWEVDTEGNYDYLMYADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240

QY 241 FSFPDMLSYRSQTKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300
Db 241 FSFPDMLSYRSQTKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300

QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVNDHTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVNDHTEPGQALQSWDPWFKPLAYAFILTRQEG 360

QY 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDGP GSKWYVKGQHAGKVFDYDLTCNRS DTVTINS DCGWGEFKVNGGSVSW 480
Db 421 GSGLAALITDGP GSKWYVKGQHAGKVFDYDLTCNRS DTVTINS DCGWGEFKVNGGSVSW 480

QY 481 VPRKTTVSTTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTTIARPIITTRPWTGFEFVRWTEPRLVAMP 515

RESULT 2
AAW31406
ID AAW31406 standard; protein; 515 AA.
XX
AC AAW31406;
XX
DT 17-OCT-2003 (revised)
DT 11-MAY-1998 (first entry)
XX
DE Bacillus stearothermophilus Termamyl-like alpha-amylase.
XX
KW Termamyl; alpha-amylase; enzyme engineering; protein engineering; starch;
KW liquefaction; saccharification; sweetener; detergent; textile desizing;
KW detergent additive; ss.
XX
OS Geobacillus stearothermophilus.
XX
PN WO9741213-A1.
XX
PD 06-NOV-1997.
XX
PF 30-APR-1997; 97WO-DK000197.
XX
PR 30-APR-1996; 96DK-00000515.
PR 28-JUN-1996; 96DK-00000712.
PR 11-JUL-1996; 96DK-00000775.
PR 08-NOV-1996; 96DK-00001263.
```

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XX
PA (NOVO ) NOVO-NORDISK AS.
PI
XX
SV Svendsen A, Borchert TV, Bisgard-Frantzen H;
DR WPI; 1997-549718/50.
DR N-PSDB; AAV02473.
XX
PT Termamyl-like alpha-amylase variants with improved properties - e.g.
PT increased stability at low pH and low calcium, useful as detergent
PT additives and in industrial starch processing e.g. liquefaction.
XX
PS Disclosure; Page 86; 101pp; English.
XX
CC This protein comprises the Termamyl-like alpha-amylase of Bacillus
CC steatothermophilus. The invention relates to novel variants of Termamyl-
CC like alpha-amylases that have alpha-amylase activity and exhibit an
CC alteration in at least one property selected from: substrate specificity;
CC binding or cleavage pattern; thermal stability; pH/activity or
CC pH/stability profile; stability towards oxidation; Ca2+ dependency and
CC specific activity. The variant has one or more mutations from those
CC listed in the specification in relation to Bacillus licheniformis
CC Termamyl (see AAW31404). Also claimed are constructs comprising DNA
CC encoding the variant (see AAV02471-73), and recombinant expression
CC vectors and transformed cells containing the DNA. The Termamyl-like alpha
CC -amylase variant is useful as a detergent additive and can also be used
CC in industrial starch processing e.g. liquefaction (claimed) or
CC saccharification to produce sweeteners, and in textile desizing
CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 515 AA;

Query Match      100.0%; Score 2854; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANNLSLIGITALWLPAYKGTSRSDVG YVY 60
Db 1 AAFPNGTMMQYFEWLPDDGTLTKVANEANNLSLIGITALWLPAYKGTSRSDVG YVY 60

QY 61 DLYDLGEFNQKGTVRTKYGTKAQYLOAQIAAHAAGM QYVADVDFDHKGADGTEWDAVE 120
Db 61 DLYDLGEFNQKGTVRTKYGTKAQYLOAQIAAHAAGM QYVADVDFDHKGADGTEWDAVE 120

QY 121 VNPSDRNQEISGTQYIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
Db 121 VNPSDRNQEISGTQYIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180

QY 181 IGKAWDWEVDTEGNYDYLMYADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240
Db 181 IGKAWDWEVDTEGNYDYLMYADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240

QY 241 FSFPDMLSYRSQTKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300
Db 241 FSFPDMLSYRSQTKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300

QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVNDHTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVNDHTEPGQALQSWDPWFKPLAYAFILTRQEG 360

QY 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDGP GSKWYVKGQHAGKVFDYDLTCNRS DTVTINS DCGWGEFKVNGGSVSW 480
Db 421 GSGLAALITDGP GSKWYVKGQHAGKVFDYDLTCNRS DTVTINS DCGWGEFKVNGGSVSW 480

QY 481 VPRKTTVSTTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
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RESULT 3
AA99770
ID AA99770 standard; protein; 515 AA.
XX
AC
AA99770;
XX
DT 12-SEP-2003 (revised)
DT 04-SEP-2000 (first entry)
DE
DE Bacillus stearothermophilus Termamyl-like alpha-amylase #2.
XX
KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
KW saccharification; muten; mutant; enzyme stability; hybrid.
XX
OS
Geobacillus stearothermophilus.
XX
PN WC200029560-A1.
XX
PD 25-MAY-2000.
XX
PF 16-NOV-1999; 99WO-DK000628.
XX
PR 16-NOV-1998; 98DK-00001495.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
XX
DR WPI; 2000-38777/33.
DR N-PSDB; AAA4842.
XX
PT Variant of parent termamyl-like alpha amylase useful for washing, textile
PT desizing and starch liquefaction, comprising alterations in one or more
PT solvent exposed amino acid residues.
XX
PS Claim 8; Fig 1; 80pp; English.
XX
CC The present sequence is a parent alpha-amylase from which mutants with
CC increased stability at acidic pH, low calcium concentration and high
CC temperatures have been derived. A variant may contain mutations in one or
CC more solvent exposed amino acid residues to increase the overall
CC hydrophobicity of the enzyme or the overall number of methyl groups in
CC the side chains of exposed residues may be increased. The mutations can
CC be incorporated by site-directed mutagenesis or by random mutagenesis. As
CC a result of their increased stability, the variants are suitable for the
CC industrial processing of starch, i.e. starch liquefaction and
CC saccharification. They may also be useful for washing, dishwashing and
CC textile desizing. Hybrid alpha-amylases comprising partial amino acid
CC sequences derived from two or more alpha-amylases have also been created
CC in order to increase enzyme stability. Note: According to the
CC specification, the present sequence and the sequence shown in AA999604
CC are the same. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 3; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMOYFEWYLPDDGTLTKVANEANNSLGLITALLWLPAYKGTSRSDVGYGVY 60
DB 1 AAPFNGTMOYFEWYLPDDGTLTKVANEANNSLGLITALLWLPAYKGTSRSDVGYGVY 60

QY 61 DLVDLGEFNGKGTVRTKYGKCAQVLOIAAHAGMOMVYADVDFDHKGADGTSEWDAVE 120
DB 61 DLVDLGEFNGKGTVRTKYGKCAQVLOIAAHAGMOMVYADVDFDHKGADGTSEWDAVE 120

QY 121 VNPSDRNOEISGTYQIQAWTKFDPGKGTYSSEFKRWYHFDGVDWDESKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTYQIQAWTKFDPGKGTYSSEFKRWYHFDGVDWDESKLSRIYKFRG 180

QY 181 IGRANDWEVDTEGNGDYLYADLMDHPEVVTTELKNWGWYNTTNDGFRDLDAVKHIK 240
DB 181 IGRANDWEVDTEGNGDYLYADLMDHPEVVTTELKNWGWYNTTNDGFRDLDAVKHIK 240

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CC as fuel, drinking and industrial ethanol production, desizing of
CC textiles, fabrics or garments. (I) exhibits a reduced capability of
CC cleaving a substrate close to the branching point, and further exhibits
CC improved substrate specificity and/or improved specific activity relative
CC to the parent alpha-amylase. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60
DB 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60
QY 61 DLYDLGEFNGQGTVRTKYGTKAQYLQALQAAHAAGMOMYADVDFDHKGADGTEWDAVE 120
DB 61 DLYDLGEFNGQGTVRTKYGTKAQYLQALQAAHAAGMOMYADVDFDHKGADGTEWDAVE 120
QY 121 VNPSDRNQEISGTVOIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
DB 121 VNPSDRNQEISGTVOIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
QY 181 ICKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240
DB 181 ICKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240
QY 241 FSFPFDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLDAPLHNKFTYASK 300
DB 241 FSFPFDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLDAPLHNKFTYASK 300
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
DB 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
QY 421 GSGLAALITDGPGGSKWYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
DB 421 GSGLAALITDGPGGSKWYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
QY 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
DB 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515

RESULT 5

ID ABB06935 standard; protein; 515 AA.

XX ABB06935;

AC ABB06935;

XX 29-AUG-2003 (revised)

DT 19-JUN-2002 (first entry)

XX B. steaerothermophilus termamyl-like alpha-amylase protein SEQ ID NO:6.

XX Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
KW washing; sweetener; ethanol; starch.

XX Geobacillus steaerothermophilus.

XX WO200166712-A2.

XX 13-SEP-2001.

XX 07-MAR-2001; 2001WO-DK000144.

XX

PR 08-MAR-2000; 2000DK-00000376.
PR 15-MAR-2000; 2000US-0189857P.
PR 23-FEB-2001; 2001DK-00000303.
PR 26-FEB-2001; 2001US-0271382P.
XX
PA (NOVO) NOVOZYMES AS.

XX Andersen C, Borchert TV, Nielsen BR;
PI
XX WPI; 2002-239612/29.
DR N-PSDB; ABL50566.

XX Novel variant of parent termamyl-like alpha-amylase useful as a component
PT in washing and dishwashing compositions, for textile desizing, for starch
PT liquefaction, and for producing sweeteners and ethanol from starch.

XX Claim 8; Page 138-139; 153pp; English.

XX The present invention describes a variant of a parent termamyl-like alpha
CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
CC positions of a group of 31 possible amino acid positions. The alteration
CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
CC washing and/or dishwashing, textile desizing, and starch liquefaction.
CC (I) is useful as a component in hard surface cleaning detergent
CC composition, and for producing sweeteners and ethanol from starch. (I)
CC has altered solubility, preferably increased solubility, in particular
CC under washing, dish washing or hard surface cleaning conditions. The
CC present sequence represents a Bacillus steaerothermophilus termamyl-like
CC alpha-amylase which is used in the exemplification of the present
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 5; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60
DB 1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLGLTALWLPAYKGTSRSDVGYGVY 60
QY 61 DLYDLGEFNGQGTVRTKYGTKAQYLQALQAAHAAGMOMYADVDFDHKGADGTEWDAVE 120
DB 61 DLYDLGEFNGQGTVRTKYGTKAQYLQALQAAHAAGMOMYADVDFDHKGADGTEWDAVE 120
QY 121 VNPSDRNQEISGTVOIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
DB 121 VNPSDRNQEISGTVOIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
QY 181 ICKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240
DB 181 ICKAWDEVDTEGNGYDLYMTADLMDHPEVVTTELKNGWKYVNTNIDGFRDLDAVKHIK 240
QY 241 FSFPFDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLDAPLHNKFTYASK 300
DB 241 FSFPFDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLDAPLHNKFTYASK 300
QY 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
DB 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
QY 421 GSGLAALITDGPGGSKWYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
DB 421 GSGLAALITDGPGGSKWYVKGQHAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
QY 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515

Db	481	VPRKTTVTSTIARPIITRPWTGFEVVRTEPRLVAMP	515
Db	121	VNPSSDRNQEISGTQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Db	121	VNPSSDRNQEISGTQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Qy	181	IGKAWDEVDVTENGNDYDLYMYADLMDHPEVVTTELKXWGWYNTTNDGFRDLDAVKHIK	240
Db	181	IGKAWDEVDVTENGNDYDLYMYADLMDHPEVVTTELKXWGWYNTTNDGFRDLDAVKHIK	240
Qy	241	FSFFPDWLSYVRSQTKPLFTVGEYNSYDINKLHNITTKDGTMSLFDAPLHNKFTYASK	300
Db	241	FSFFPDWLSYVRSQTKPLFTVGEYNSYDINKLHNITTKDGTMSLFDAPLHNKFTYASK	300
Qy	301	SGGAFDMRTLMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWVDWPFKPLAYAFILTRQEG	360
Db	301	SGGAFDMRTLMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWVDWPFKPLAYAFILTRQEG	360
Qy	361	YPCVFYGDYIGIPOYNIPLSKIDPLLIARRIAYGTQHDYLDHSDIIGWTREGGTEKP	420
Db	361	YPCVFYGDYIGIPOYNIPLSKIDPLLIARRIAYGTQHDYLDHSDIIGWTREGGTEKP	420
Qy	421	GSGLAALITDGPSSKWMYVKGQHAGKVFYDLTGNSRSDTVTINSDDGWFVKVNGSVSW	480
Db	421	GSGLAALITDGPSSKWMYVKGQHAGKVFYDLTGNSRSDTVTINSDDGWFVKVNGSVSW	480
Qy	481	VPRKTTVTSTIARPIITRPWTGFEVVRTEPRLVAMP	515
Db	481	VPRKTTVTSTIARPIITRPWTGFEVVRTEPRLVAMP	515
RESULT 7			
AAAB47852			
ID	AAAB47852	standard; protein; 515 AA.	
AC	AAAB47852;		
XX			
DT	29-AUG-2003	(revised)	
DT	02-APR-2002	(first entry)	
DE	Bacillus alpha amylase BSG.		
XX			
XX	Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;		
KW	starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;		
KW	bakery; cereal bar; ice cream; coffee whitener; salad dressing;		
XX	cured meat; fermented meat; spice.		
OS	Geobacillus stearothermophilus.		
XX			
PN	WO200196537-A2.		
XX			
PD	20-DEC-2001.		
XX			
XX	13-JUN-2001; 2001WO-DK000404.		
XX	14-JUN-2000; 2000DK-00000917.		
PR	20-JUN-2000; 2000US-0212852P.		
XX			
FA	(NOVO) NOVOZYMES AS.		
XX			
PI	Nielsen BR, Weibye M;		
XX			
DR	WPI; 2002-098064/13.		
DR	N-PSDB; AAI72213.		
XX			
PT	New modified alpha-amylase derived from the genus Bacillus and/or is a		
PT	Termamyl-like alpha-amylase, which has been pre-oxidized for producing		
PT	maltodextrin or glucose syrup.		
XX			
PS	Claim 5; Page 32-33; 47pp; English.		
XX			
CC	The sequences given in AAB47850-56 show modified alpha-amylases derived		
CC	from the genus Bacillus. These alpha amylases are Termamyl-like alpha-		
CC	amylase and they have been pre-oxidized. The alpha amylase is useful for		

Db	AAU12151	standard; protein; 515 AA.	
XX	AAU12151.		
XX	29-AUG-2003	(revised)	
DT	09-APR-2002	(first entry)	
XX			
DE	Bacillus TERMAMYL-like alpha-amylase BSG.		
XX			
KW	TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;		
KW	starch liquefaction; ethanol production; hard surface cleaner; sweetener;		
KW	amylpectin; limit dextrin; NOVAMYL; BSG.		
OS	Geobacillus stearothermophilus.		
XX			
PN	WO200188107-A2.		
XX			
PD	22-NOV-2001.		
XX			
XX	10-MAY-2001; 2001WO-DK000323.		
XX			
PR	12-MAY-2000; 2000DK-00000779.		
XX			
PA	(NOVO) NOVOZYMES AS.		
XX			
PI	Svendsen A, Jorgensen CT, Nielsen BR;		
XX			
DR	WPI; 2002-106123/14.		
DR	N-PSDB; AAS20024.		
XX			
PT	New variant of parent Termamyl-like alpha-amylase for use as a component		
PT	in washing and dishwashing compositions, for textile desizing, for starch		
PT	liquefaction, and for producing sweeteners and ethanol from starch.		
XX			
PS	Claim 5; Fig 1; 84pp; English.		
XX			
CC	The invention relates to a variant of parent TERMAMYL-like alpha- amylase		
CC	comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,		
CC	or at position 234, where the variant has alpha-amylase activity and each		
CC	position corresponds to a position of a parent Termamyl-like alpha-		
CC	amylase sequence having a Bacillus licheniformis alpha-amylase sequence		
CC	of 483 amino acids, given in specification. The variant alpha- amylase, a		
CC	detergent additive comprising the variant or a detergent composition		
CC	comprising the variant, is useful for washing and/or dishwashing or		
CC	textile desizing. The alpha-amylase is useful for starch liquefaction or		
CC	ethanol production and as a component in a hard surface cleaning		
CC	detergent composition, and for producing sweeteners from starch. The		
CC	variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage		
CC	activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic		
CC	branch linkage cleavage activity of amylopectin or a limit dextrin		
CC	prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a		
CC	natural variant of the TERMAMYL alpha-amylase, BSG. (Updated on 29-AUG-		
CC	2003 to standardise OS field)		
XX			
SQ	Sequence 515 AA;		
Query Match	100.0%; Score 2854; DB 5; Length 515;		
Best Local Similarity	100.0%; Pred. No. 7.4e-246;		
Matches 515; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	AAPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALTALWLPAYKGTSRSDVGXGVY	60
Db	1	AAPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALTALWLPAYKGTSRSDVGXGVY	60
Qy	61	DLVDLGEFNQKGTVRTKYTKAQYLOAIQAAHAGMOMVYADVPDHPKGGADGTETWDAVE	120
Db	61	DLVDLGEFNQKGTVRTKYTKAQYLOAIQAAHAGMOMVYADVPDHPKGGADGTETWDAVE	120

CC producing a maltodextrin or glucose syrup, by treating starch with a pre-oxidized alpha-amylase until a product with a DE between 5-45 has been provided and/or until a product with a molecular weight of between 5-30 kDa has been provided. The product comprises a maltodextrin with a DE of 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The alpha amylase is useful for producing a maltodextrin or glucose syrup, where the glucose syrup is useful as an ingredient in food, feed or pharmaceuticals. Glucose syrup is useful in confectionery such as candies, beverages such as isotonic drinks, bakery such as cereal bars, dairy and ice cream such as coffee whiteners, conventional foods such as salad dressings, and food ingredients and preparations such as cured meat, fermented meat, spices and seasoning encapsulated flavours. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 5; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60
DB 1 AAPPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60
QY 61 DLYDLGEFNGKGTVRTKYTKAQYLOAQAAHAAGMQYADVDFHKGADGTEWDAVE 120
DB 61 DLYDLGEFNGKGTVRTKYTKAQYLOAQAAHAAGMQYADVDFHKGADGTEWDAVE 120
QY 121 VNPSDRNQEISGTYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
DB 121 VNPSDRNQEISGTYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
QY 181 IGKAWDWEVDTEGNYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240
DB 181 IGKAWDWEVDTEGNYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240
QY 241 FSFPFDWLSYRSQTKPLFTVGEYNSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300
DB 241 FSFPFDWLSYRSQTKPLFTVGEYNSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300
QY 301 SGGA FDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360
DB 301 SGGA FDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360
QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420
DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420
QY 421 GSGLAALITDGP GSKWYVKGQHAGKVFDLTGNRSDTITNSDGWGEFKVNGGSVW 480
DB 421 GSGLAALITDGP GSKWYVKGQHAGKVFDLTGNRSDTITNSDGWGEFKVNGGSVW 480
QY 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515
DB 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515

RESULT 8
ABB76588

ID ABB76588 standard; protein; 515 AA.

XX ABB76588;

XX 29-AUG-2003 (revised)

DT 19-AUG-2002 (first entry)

XX Termamyl-like-alpha-amylase #3.

XX Termamyl; alpha amylase; starch liquefaction; ethanol production;
KW textile desizing; detergent; enzyme.

XX Geobacillus stearothermophilus.

PN WO200210355-A2.
XX 07-FEB-2002.
XX 12-JUL-2001; 2001WO-DK000488.
XX 01-AUG-2000; 2000DK-00001160.
PR 12-SEP-2000; 2000DK-00001354.
PR 10-NOV-2000; 2000DK-00001687.
PR 26-APR-2001; 2001DK-00000655.
XX (NOVO) NOVOZYMES AS.
XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
PI WPI; 2002-280633/32.
XX N-PSDB; ABL96209.
DR Variant of parent Termamyl-like alpha amylase, useful in detergent
XX compositions, for starch liquefaction, ethanol production, washing and/or
PT dish washing, and textile desizing.
PT Claim 4; Fig 5; 90pp; English.
XX This invention relates to variants of a parent Termamyl-like alpha-
CC amylases. These are used for starch liquefaction, ethanol production,
CC detergent, and textile desizing. The amylases have altered stability,
CC particularly at high temperatures from 70-120plusOC and low pH in the
CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
CC amylase. (Updated on 29-AUG-2003 to standardise OS field)
XX Sequence 515 AA;

Query Match 100.0%; Score 2854; DB 5; Length 515;
Best Local Similarity 100.0%; Pred. No. 7.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAPPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60
DB 1 AAPPNGTMMQYFEWYLPDDGTLWTKVANEANLSSLGITALLWLPAYKGTSDVGYGY 60
QY 61 DLYDLGEFNGKGTVRTKYTKAQYLOAQAAHAAGMQYADVDFHKGADGTEWDAVE 120
DB 61 DLYDLGEFNGKGTVRTKYTKAQYLOAQAAHAAGMQYADVDFHKGADGTEWDAVE 120
QY 121 VNPSDRNQEISGTYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
DB 121 VNPSDRNQEISGTYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
QY 181 IGKAWDWEVDTEGNYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240
DB 181 IGKAWDWEVDTEGNYDYLMDHDPVETLKNWGWYVNTTNDGFRDLDAVKHIK 240
QY 241 FSFPFDWLSYRSQTKPLFTVGEYNSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300
DB 241 FSFPFDWLSYRSQTKPLFTVGEYNSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300
QY 301 SGGA FDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360
DB 301 SGGA FDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360
QY 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420
DB 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420
QY 421 GSGLAALITDGP GSKWYVKGQHAGKVFDLTGNRSDTITNSDGWGEFKVNGGSVW 480
DB 421 GSGLAALITDGP GSKWYVKGQHAGKVFDLTGNRSDTITNSDGWGEFKVNGGSVW 480
QY 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515
DB 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRLVAMP 515

CC baking processes, beverages, oil fields (fuel ethanol), brewing processes
CC and starch modification in the paper and pulp industry, for removing
CC starch containing stains from a material and for reducing staling of
CC bakery products. Sequences ABU03040-ABU03144 represent alpha amylase
CC polypeptides of the invention
XX
SQ Sequence 549 AA;

Query Match 99.4%; Score 2836; DB 6; Length 549;
Best Local Similarity 99.4%; Pred. No. 3.3e-244;
Matches 512; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITALMLPPAYKGTSRSDVGYY 60
Db 35 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITALMLPPAYKGTSRSDVGYY 94

Qy 61 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGMOMVADVPDHHKGGADGTWDAVE 120
Db 95 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGMOMVADVPDHHKGGADGTWDAVE 154

Qy 121 VNFSDRNQEIISGTYQIQAWTKFDPGRGNTYSGFKRWYHFDGVDWDESRKLSRIYKFRG 180
Db 155 VNFSDRNQEIISGTYQIQAWTKFDPGRGNTYSGFKRWYHFDGVDWDESRKLSRIYKFRG 214

Qy 181 IGKAWDWEVDTEGNYDYLMAVDLMDHPEVVTTELKNWGWYNTTNDGFRDLDAVKHIK 240
Db 215 IGKAWDWEVDTEGNYDYLMAVDLMDHPEVVTTELKNWGWYNTTNDGFRDLDAVKHIK 274

Qy 241 FSFPDMLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 300
Db 275 FSFPDMLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 334

Qy 301 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPPWPKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPPWPKPLAYAFILTRQEG 394

Qy 361 YPCVFYGDYIGIPQYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420
Db 395 YPCVFYGDYIGIPQYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 454

Qy 481 VPRKTTVSTIARPIITRPWTGFEVVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITRPWTGFEVVRWTEPRLVAMP 549

RESULT 11
ABU03084
ID ABU03084 standard; protein; 549 AA.
XX
AC ABU03084;
XX
DT 21-JAN-2003 (first entry)
XX
DE Alpha amylase polypeptide #45.
XX
KW Alpha amylase; enzyme; starch linkage hydrolysis; starch liquefaction;
KW starch breakdown catalysis; textile desizing; lignocellulosic fibre;
KW enzymatic de-inking; recycled paper; high-maltose syrup; dough;
KW high glucose syrup; corn-wet milling process; detergent; baking process;
KW beverage; oil field; fuel ethanol; brewing process; staling;
KW starch modification.
XX
OS Unidentified.
XX
PN WO200268589-A2.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005068.

XX 21-FEB-2001; 2001US-0270495P.
PR 21-FEB-2001; 2001US-0270496P.
PR 14-MAY-2001; 2001US-0291122P.
XX
PA (DIVE-) DIVERSA CORP.
XX
PI Callen W, Richardson T, Frey G;
XX WPI; 2003-018656/01.
DR N-PSDB; ABX08455.
XX
PT Novel purified polypeptide with alpha-amylase activity, useful e.g. for
PT liquefying starch, for textile desizing, for treating lignocellulosic
PT fibers, and for producing high-maltose or high-glucose syrup.
XX
PS Claim 30; Fig 16; 30pp; English.
XX
CC The invention relates to a purified polypeptide with alpha-amylase
CC activity and the polynucleotide encoding it. The polypeptide is useful
CC for hydrolysing starch linkages, for catalysing the breakdown of a
CC starch, for modifying small molecules, for liquefying starch, for washing
CC an object, for textile desizing, for treating lignocellulosic fibers, for
CC improving fibre properties, for enzymatic de-inking of recycled paper
CC pulp, for producing a high-maltose or high-glucose syrup or a mixed
CC subterranean formation by removing a viscous, starch-containing, damaging
CC fluid formed during production operations and found within the
CC subterranean formation which surrounds a completed well bore. The
CC polypeptide is also useful for preparing a dough or a baked product
CC prepared from the dough and in corn-wet milling processes, detergents,
CC baking processes, beverages, oil fields (fuel ethanol), brewing processes
CC and starch modification in the paper and pulp industry, for removing
CC starch containing stains from a material and for reducing staling of
CC bakery products. Sequences ABU03040-ABU03144 represent alpha amylase
CC polypeptides of the invention
XX
SQ Sequence 549 AA;

Query Match 99.2%; Score 2832; DB 6; Length 549;
Best Local Similarity 99.4%; Pred. No. 7.5e-244;
Matches 512; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITALMLPPAYKGTSRSDVGYY 60
Db 35 AAPFNGTMQYFEWYLPDDGTLTKVANEANLSSLGITALMLPPAYKGTSRSDVGYY 94

Qy 61 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGMOMVADVPDHHKGGADGTWDAVE 120
Db 95 DLYDLGEFNQKGTVRTKYGTAQYLOAIQAAHAGMOMVADVPDHHKGGADGTWDAVE 154

Qy 121 VNFSDRNQEIISGTYQIQAWTKFDPGRGNTYSGFKRWYHFDGVDWDESRKLSRIYKFRG 180
Db 155 VNFSDRNQEIISGTYQIQAWTKFDPGRGNTYSGFKRWYHFDGVDWDESRKLSRIYKFRG 214

Qy 181 IGKAWDWEVDTEGNYDYLMAVDLMDHPEVVTTELKNWGWYNTTNDGFRDLDAVKHIK 240
Db 215 IGKAWDWEVDTEGNYDYLMAVDLMDHPEVVTTELKNWGWYNTTNDGFRDLDAVKHIK 274

Qy 241 FSFPDMLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 300
Db 275 FSFPDMLSVRSQTKPLFTVGEWYSYDINKLHNYITKTGTMSLFDAPLHNKFTASK 334

Qy 301 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPPWPKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTLMTNTLMKQOPTLAVTFVDNHDTEPGQALQSWDPPWPKPLAYAFILTRQEG 394

Qy 361 YPCVFYGDYIGIPQYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 420
Db 395 YPCVFYGDYIGIPQYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGTEKP 454
Qy 421 GSGLAALITDGPGGSKWYVGKHAGKVPYDLTGNSDVTITNSDGMGEKFGKNGSVSW 480
|||||

Qy 61 DLYDLGEBFNQKGTVRTTKYGTAKQYLQAIQAAHAAGMOMVYADVDPDHKGGADGTETWDAVE 120
Dy 61 DLYDLGEBFNQKGTVRTTKYGTAKQYLQAIQAAHAAGMOMVYADVDPDHKGGADGTETWDAVE 120
Qy 121 VNPSDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Dy 121 VNPSDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Qy 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNWGWYNTTNIIDGFRDLDAVKHIK 240
Dy 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNWGWYNTTNIIDGFRDLDAVKHIK 240
Qy 241 FSPFPDMLSVYRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300
Dy 241 FSPFPDMLSVYRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300
Qy 301 SGGAFDMRTLMNTLMKDQPTLAVTFVNDHDETEPGQALQSWDPWFKPLAYAFILTRQEG 360
Dy 301 SGGAFDMRTLMNTLMKDQPTLAVTFVNDHDETEPGQALQSWDPWFKPLAYAFILTRQEG 360
Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Dy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Qy 421 GSGLAALITDGPGGSKMWMYVGHQAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
Dy 421 GSGLAALITDGPGGSKMWMYVGHQAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
Qy 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
Dy 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
RESULT 14
AAW48263
ID AAW48263 standard; protein; 515 AA.
AC AC
XX AAW48263;
DT 02-JUL-1998 (first entry)
DE Bacillus sp. alpha amylase protein #3.
KW Alpha amylase; stain digestion; detergent; fabric laundry performance.
OS Bacillus sp.
PN WO9805748-A1.
PD 12-FEB-1998.
PF 01-AUG-1996; 96WO-US012612.
XX 01-AUG-1996; 96WO-US012612.
PR (PROC) PROCTER & GAMBLE CO.
XX Baech AC, Jones LA, Ohtani R, Pramod K, Rai S, Showell MS;
XX WPI; 1998-159168/14.
PT Use of specific alpha-amylase enzymes - in laundry detergent compositions
PT to provide effective cleaning and whitening of dingy fabrics.
XX Claim 1; Page 74; 82pp; English.
PS This sequence represents an alpha amylase from Bacillus sp. which is used
CC in a laundry detergent. The detergent compositions can be used for
CC boosting fabric laundry performance or for dingy fabric cleanup
XX Sequence 515 AA;
SQ

Query Match 97.7%; Score 2787; DB 2; Length 515;
Best Local Similarity 98.1%; Pred. No. 7.2e-240;
Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
Qy 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSIGITALLWLPAYKGTFSRSDVGYY 60
Dy 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSIGITALLWLPAYKGTFSRSDVGYY 60
Qy 61 DLYDLGEBFNQKGTVRTTKYGTAKQYLQAIQAAHAAGMOMVYADVDPDHKGGADGTETWDAVE 120
Dy 61 DLYDLGEBFNQKGTVRTTKYGTAKQYLQAIQAAHAAGMOMVYADVDPDHKGGADGTETWDAVE 120
Qy 121 VNPSDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Dy 121 VNPSDRNOEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Qy 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNWGWYNTTNIIDGFRDLDAVKHIK 240
Dy 181 IGKAWDEVDTEGNYDYLMDADLMDHPEVVTTELKNWGWYNTTNIIDGFRDLDAVKHIK 240
Qy 241 FSPFPDMLSVYRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300
Dy 241 FSPFPDMLSVYRSOTGKPLFTVGYWYSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300
Qy 301 SGGAFDMRTLMNTLMKDQPTLAVTFVNDHDETEPGQALQSWDPWFKPLAYAFILTRQEG 360
Dy 301 SGGAFDMRTLMNTLMKDQPTLAVTFVNDHDETEPGQALQSWDPWFKPLAYAFILTRQEG 360
Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Dy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Qy 421 GSGLAALITDGPGGSKMWMYVGHQAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
Dy 421 GSGLAALITDGPGGSKMWMYVGHQAGKVFYDLTGNSRSDTVTINS DGWGEFKVNGGSVSW 480
Qy 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
Dy 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515
RESULT 15
AAW25153
ID AAW25153 standard; protein; 515 AA.
AC AC
XX AAW25153;
DT 27-AUG-1999 (first entry)
DE Bacillus sp. alpha-amylase protein fragment 3.
KW Alpha-amylase; cleaning composition; protease variant; spot removal;
KW detergent composition; hard surface cleaning; fabric cleaning;
KW dishwashing composition; oral cleaning composition; personal cleansing;
KW stain removal; soil removal; whiteness maintenance; dingy cleanup;
KW film removal.
OS Bacillus sp.
XX WO9920723-A2.
PN 29-APR-1999.
PD 23-OCT-1998; 98WO-US022486.
XX 23-OCT-1997; 97US-00956323.
PR 23-OCT-1997; 97US-00956324.
XX 23-OCT-1997; 97US-00956564.
PA (PROC) PROCTER & GAMBLE CO.
XX Ghosh CK, Baech AC, Ohtani R, Busch A, Showell MS;
XX

DR WPI; 1999-404706/34.
XX
PT Cleaning compositions used in e.g. detergent for cleaning hard surfaces
PT or fabrics, dishwashing or oral cleaning comprises protease and amylase
PT variants having amino acid residues.
XX
PS Claim 1b(viii); Page 169; 169pp; English.
PS
XX
CC This invention describes novel cleaning compositions which contain a
CC protease variant with an amino acid substitution corresponding to
CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.
CC The compositions can be used in e.g. detergent compositions, for cleaning
CC hard surfaces or fabrics, dishwashing compositions, oral cleaning
CC compositions, detergent cleaning compositions and personal cleansing
CC compositions. The combination of protease variants and alpha-amylase
CC variants in cleaning compositions can provide improved and enhanced
CC cleaning ability, including stain and/or soil removal and/or reduction
CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or film
CC removal and/or reduction, over conventional enzyme-containing cleaning
CC compositions
XX
SQ Sequence 515 AA;

Query Match 97.7%; Score 2787; DB 2; Length 515;
Best Local Similarity 98.1%; Pred. No. 7.2e-240;
Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 AAPFNGTMMQYFEWYLPDDGLTWKVAEANNLSSLGITALLWLPAYKTSRSDVGYG 60
DB 1 AAPFNGTMMQYFEWYLPDDGLTWKVAEANNLSSLGITALLWLPAYKTSRSDVG 60

QY 61 DLYDLGEFNGKGVRTKYTKAQVQLQIAAHAGMQVYADVDFDHKGADGTETWDAVE 120
DB 61 DLYDLGEFNGKGVRTKYTKAQVQLQIAAHAGMQVYADVDFDHKGADGTETWDAVE 120

QY 121 VNPSDRNQEISGTQIOAWTKFDPGRGNTYSSFKWYHFDGVDWDESRKLSRIYKFRG 180
DB 121 VNPSDRNQEISGTQIOAWTKFDPGRGNTYSSFKWYHFDGVDWDESRKLSRIYKFRG 180

QY 181 IGRADWEVDTEGNGYDLYADLDMDHPEVVTLEKNWGWYVNTTIDGFRDLDAVKHIK 240
DB 181 IGRADWEVDTEGNGYDLYADLDMDHPEVVTLEKNWGWYVNTTIDGFRDLDAVKHIK 240

QY 241 FSFPFDWLSYRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300
DB 241 FSFPFDWLSYRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK 300

QY 301 SGGAFTMRTLTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDWPFKPLAYAFILTRQEG 360
DB 301 SGGAFTMRTLTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDWPFKPLAYAFILTRQEG 360

QY 361 YPCVFYGDYVYGIPOYNIPSLKSDPLLIARDYAYGTOHDYLDHSDIIGWTREGGTEKP 420
DB 361 YPCVFYGDYVYGIPOYNIPSLKSDPLLIARDYAYGTOHDYLDHSDIIGWTREGGTEKP 420

QY 421 GSGLAALITDQPGGSKWYVCKQKAGKVFYDLTGNSRSDTITNSDGMGEFKVNGSGSVW 480
DB 421 GSGLAALITDQPGGSKWYVCKQKAGKVFYDLTGNSRSDTITNSDGMGEFKVNGSGSVW 480

QY 481 VPRKTTVSTIARPTTRPTWGEFVRWTEPRLVAMP 515
DB 481 VPRKTTVSTIARPTTRPTWGEFVRWTEPRLVAMP 515

Search completed: October 7, 2004, 00:12:16
Job time : 65.1733 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 15.8068 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-6

Perfect score: 2854

Sequence: 1 AAPFNCTMQYFEWYLPDDG.....TRPWTGEFVWTEPRLVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2854	100.0	549	1 A54541	alpha-amylase (EC
2	2812	98.5	549	1 A24549	alpha-amylase (EC
3	2787	97.7	549	1 A24436	alpha-amylase (EC
4	2727.5	95.6	548	1 ALBSF	alpha-amylase (EC
5	1874.5	65.7	518	1 A27705	alpha-amylase (EC
6	1794.5	62.9	512	1 ALBSL	alpha-amylase (EC
7	1773.5	62.1	514	1 ALBSN	alpha-amylase (EC
8	1345.5	47.1	492	2 RH2079	alpha-amylase (imp
9	1315	46.1	484	2 G95160	alpha-amylase (imp
10	1311	45.9	484	2 F98026	alpha-amylase (EC
11	1278.5	44.8	493	2 S15713	alpha-amylase (EC
12	1229	43.1	491	2 C86781	alpha-amylase (imp
13	1112.5	39.0	494	1 B45738	alpha-amylase (EC
14	1101.5	38.6	494	2 AD0751	cytoplasmic alpha-
15	1078.5	37.8	495	2 AD3038	alpha-amylase (imp
16	1078.5	37.8	506	2 G98247	cytoplasmic alpha-
17	1074.5	37.6	495	1 A45738	alpha-amylase (EC
18	1074.5	37.6	495	2 B90962	cytoplasmic alpha-
19	1055.5	37.0	495	2 B85810	cytoplasmic alpha-
20	354.5	12.4	217	2 AL9506	alpha-amylase (EC
21	326.5	11.4	482	2 S31478	alpha-amylase (EC
22	313	11.0	713	1 ALBSG7	cyclomaltodextrin
23	307	10.8	826	2 E29130	probable alpha-amyl
24	307	10.8	1196	2 A29130	beta-amylase (EC 3
25	302.5	10.6	440	2 S14958	alpha-amylase (EC
26	302	10.6	713	2 S09196	cyclomaltodextrin
27	300	10.5	713	2 A58800	cyclomaltodextrin
28	296	10.4	423	2 T09942	alpha-amylase (EC
29	295	10.3	428	2 T05521	alpha-amylase (EC

RESULT 1

A54541

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI1792)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C;Accession: A54541

R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.

FEMS Microbiol. Lett. 77, 271-276, 1991

A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.

A;Reference number: A54541

A;Accession: A54541

A;Molecule type: DNA

A;Residues: 1-549 <IOR>

A;Cross-references: GB:X59476

A;Experimental source: Chromosomal DNA of strain DNI1792

C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the

C;Genetics:

A;Start codon: GTG

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycoen/starch degradation

C;Superfamily: alpha-amylase, amyliofaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polyacac

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-549/Product: alpha-amylase #status predicted <MAT>

F;235-368/Domain: alpha-amylase core homology <AMY>

F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2854; DB 1; Length 549;

Best Local Similarity 100.0%; Pred. No. 2.3e-198; Mismatches 0; Indels 0; Gaps 0;

Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPFNCTMQYFEWYLPDDGTLTKVANEANNLSLGLTALWLPAYKTSRSDVGQYV 60

Db 35 AAPFNCTMQYFEWYLPDDGTLTKVANEANNLSLGLTALWLPAYKTSRSDVGQYV 94

Qy 61 DLVDLGFBNQKGVTRTKYTKAQYLQIAAHAGMQYADVDPDHKGADGTWDAVE 120

Db 95 DLVDLGFBNQKGVTRTKYTKAQYLQIAAHAGMQYADVDPDHKGADGTWDAVE 154

Qy 121 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSPKWYHFDGVDWDESKLSRIYKFRG 180

Db 155 VNPSDRNOEISGTYQIOAWTKFDPGRGNTYSSPKWYHFDGVDWDESKLSRIYKFRG 214

Qy 181 IGKAWDEVDTENGNDYLMYADLMDHPVETVTEKWKYVNTTIDGFRDLDAVKHK 240

Db 215 IGKAWDEVDTENGNDYLMYADLMDHPVETVTEKWKYVNTTIDGFRDLDAVKHK 274

Qy 241 PSFPFDLWLSYVRSOTGKPLFTVGVSWYDINKLHNYITKDTGTWLSLFDAPLHNFYASK 300

Db 241 PSFPFDLWLSYVRSOTGKPLFTVGVSWYDINKLHNYITKDTGTWLSLFDAPLHNFYASK 300

Db 275 FSFPDMLSVRSQTKPLFTVGEYMSYDINKLHNYITKTDTGMSLFDAPLHNKFTASK 334
Qy 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 420
Db 395 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 454
Qy 421 GSGLAALITDGGGSKMWYVKGQHAGKVFYDLTGNRSDTVTTNSDGGGEFKVNGGSVSW 480
Db 455 GSGLAALITDGGGSKMWYVKGQHAGKVFYDLTGNRSDTVTTNSDGGGEFKVNGGSVSW 514
Qy 481 VPRKTTVSTIARPIITTRPWTGTFVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITTRPWTGTFVRWTEPRLVAMP 549
RESULT 2
A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24549; I39501; I39770
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothe
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: A24549
A;Molecule type: DNA
A;Residues: 1-549 <GRA>
A;Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513
A;Experimental source: genomic DNA of strain NZ-3
R;Sachoh, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A;Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
A;Reference number: I39501; MUID:98139156; PMID:3257753
A;Accession: I39501
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RES>
A;Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478
A;Experimental source: strain DY-5
A;Accession: I39770
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RE2>
A;Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A;Experimental source: strain 799
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted
Query Match 98.5%; Score 2812; DB 1; Length 549;
Best Local Similarity 98.8%; Pred. No. 2.5e-195;
Matches 509; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 AAPFNGTMMQYFHWLPPDDGTLTKVANEANLSSIGITALWLPYPAYKGTSRSDVGYGYY 60
Db 35 AAPFNGTMMQYFHWLPPDDGTLTKVANEANLSSIGITALWLPYPAYKGTSRSDVGYGYY 94

Qy 61 DLYDLGEFNQKGTVRTKYGTKAQYLOAIQAAHAAGMQVYADVDFDHKGGADGTWDAVE 120
Db 95 DLYDLGEFNQKGTVRTKYGTKAQYLOAIQAAHAAGMQVYADVDFDHKGGADGTWDAVE 154
Qy 121 VNSDRNQETISGTQYQIQAQTKPDPFGNGNTYSSFKRWYHFDGVDWDESKLSRIYKPRG 180
Db 155 VNSDRNQETISGTQYQIQAQTKPDPFGNGNTYSSFKRWYHFDGVDWDESKLSRIYKPRG 214
Qy 181 IGKAWDEVDVTENGNDYLMYADLDMDHPEVVTTELKNGKWYNTTNDGFRLDVAKHIK 240
Db 215 IGKAWDEVDVTENGNDYLMYADLDMDHPEVVTTELKNGKWYNTTNDGFRLDVAKHIK 274
Qy 241 FSFPDMLSVRSQTKPLFTVGEYMSYDINKLHNYITKTDTGMSLFDAPLHNKFTASK 300
Db 275 FSFPDMLSVRSQTKPLFTVGEYMSYDINKLHNYITKTDTGMSLFDAPLHNKFTASK 334
Qy 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 420
Db 395 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 454
Qy 421 GSGLAALITDGGGSKMWYVKGQHAGKVFYDLTGNRSDTVTTNSDGGGEFKVNGGSVSW 480
Db 455 GSGLAALITDGGGSKMWYVKGQHAGKVFYDLTGNRSDTVTTNSDGGGEFKVNGGSVSW 514
Qy 481 VPRKTTVSTIARPIITTRPWTGTFVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITTRPWTGTFVRWTEPRLVAMP 549
RESULT 3
A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; I39777
R;Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Accession: A24436
A;Molecule type: DNA
A;Residues: 1-549 <NAK>
A;Cross-references: GB:M11450
A;Experimental source: plasmid pAT5
A;Note: amino end of the mature protein also determined
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39777
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-45 <RES>
A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Gene: amys
A;Genome: plasmid
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 97.7%; Score 2787; DB 1; Length 549;
 Best Local Similarity 98.1%; Pred. No. 1.66-193;
 Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNNSSLGITATLWLPAYKGTSRSDVGVY 60
 Db 35 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNNSSLGITATLWLPAYKGTSRSDVGVY 94

Qy 61 DLYDLGFEFNQKGTVRTKYGTAKQYLOAIQAAHAGMOMVYADVDFDHKGADGTWDAVE 120
 Db 95 DLYDLGFEFNQKGTVRTKYGTAKQYLOAIQAAHAGMOMVYADVDFDHKGADGTWDAVE 154

Qy 121 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
 Db 155 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214

Qy 181 IGKAWDEVDTEGNYDYLAMVADLDMDHPEVVTTELKNGKMYVNTTNDGFRDLDAVKHIK 240
 Db 215 IGKAWDEVDTEGNYDYLAMVADLDMDHPEVVTTELKNGKMYVNTTNDGFRDLDAVKHIK 274

Qy 241 FSFPFDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300
 Db 275 FSFPFDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 334

Qy 301 SGGAFDMRTLTMTNLTMLKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 360
 Db 335 SGGAFDMRTLTMTNLTMLKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 394

Qy 361 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDAYGTQHDYLDHSDIIGWTRGGTEKP 420
 Db 395 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDAYGTQHDYLDHSDIIGWTRGGTEKP 454

Qy 421 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDDGGEKFKVNGSGSVW 480
 Db 455 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDDGGEKFKVNGSGSVW 514

Qy 481 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 515
 Db 515 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 549

RESULT 4
 ALBSF
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C;Species: Bacillus stearothermophilus
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Feb-1997
 R;Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uchida, S.
 J. Biochem. 98, 95-103, 1985
 A;Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology bet
 A;Reference number: A91999; MUID:86008166; PMID:3876333
 A;Accession: A91999
 A;Molecule type: DNA
 A;Residues: 1-548 <IH1>
 A;Cross-references: GB:X02769
 A;Experimental source: plasmid PH1300 from strain DY-5
 A;Accession: B91999
 A;Molecule type: protein
 A;Residues: 35-48 <IH2>
 A;Experimental source: strain DY-5
 R;Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,
 J. Bacteriol. 164, 1182-1187, 1985
 A;Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-p
 A;Reference number: A91804; MUID:86059211; PMID:2999073
 A;Accession: pBAM101
 A;Contents: pBAM101
 A;Molecule type: DNA
 A;Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
 C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
 C;Genetics:
 A;Genome: plasmid

A;Start codon: GTG
 C;Function:
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
 C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F;1-34/Domain: signal sequence #status predicted <SIG>
 F;35-548/Product: alpha-amylase #status experimental <MAT>
 F;235-368/Domain: alpha-amylase core homology
 F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 95.6%; Score 2727.5; DB 1; Length 548;
 Best Local Similarity 96.7%; Pred. No. 3.1e-189;
 Matches 498; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

Qy 1 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNNSSLGITATLWLPAYKGTSRSDVGVY 60
 Db 35 AAPNGTMMQYFEWYLPDDGTLWTKVANEANNNSSLGITATLWLPAYKGTSRSDVGVY 94

Qy 61 DLYDLGFEFNQKGTVRTKYGTAKQYLOAIQAAHAGMOMVYADVDFDHKGADGTWDAVE 120
 Db 95 DLYDLGFEFNQKGTVRTKYGTAKQYLOAIQAAHAGMOMVYADVDFDHKGADGTWDAVE 154

Qy 121 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
 Db 155 VNPSDRNQEISGTYQIOAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214

Qy 181 IGKAWDEVDTEGNYDYLAMVADLDMDHPEVVTTELKNGKMYVNTTNDGFRDLDAVKHIK 240
 Db 215 IGKAWDEVDTEGNYDYLAMVADLDMDHPEVVTTELKNGKMYVNTTNDGFRDLDAVKHIK 274

Qy 241 FSFPFDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 300
 Db 275 FSFPFDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHNKFTYASK 334

Qy 301 SGGAFDMRTLTMTNLTMLKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 360
 Db 335 SGGAFDMRTLTMTNLTMLKQDPTLAVTFVDNHDTEPGQALQSWDPMFKPLAYAFILTRQEG 393

Qy 361 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDAYGTQHDYLDHSDIIGWTRGGTEKP 420
 Db 394 YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDAYGTQHDYLDHSDIIGWTRGGTEKP 453

Qy 421 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDDGGEKFKVNGSGSVW 480
 Db 454 GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDDGGEKFKVNGSGSVW 513

Qy 481 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 515
 Db 514 VPRKTTVSTIARPIITTPWTGFEFVRWTEPRLVAMP 548

RESULT 5
 A27705
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
 C;Species: Bacillus sp.
 C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C;Accession: A27705
 R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
 Biochem. Biophys. Res. Commun. 151, 25-31, 1988
 A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from an alkaloph
 A;Reference number: A27705; MUID:88162814; PMID:3258152
 A;Accession: A27705
 A;Molecule type: DNA
 A;Residues: 1-518 <TSU>
 A;Cross-references: GB:M18862; NID:gl42496; PIDN:AAA22231.1; PID:gl42497
 A;Experimental source: chromosomal DNA of strain 707
 A;Note: amino end of mature protein also determined
 C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
 C;Function:
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-518/Product: alpha-amylase #status experimental <WAT>
F;236-369/Domain: alpha-amylase core homology <AMY>
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 65.7%; Score 1874.5; DB 1; Length 518;
Best Local Similarity 67.2%; Pred. No. 1.1e-127;
Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;

QY 5 NGTMMQYFEWYLPDDGTLTWKVAENANSLGITALWLPAYKGRSDVGYGYDLYD 64
DB 39 NGTMMQYFEWYLPDNGNHNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGAYDLYD 98

QY 65 LGEFNQKGTVTKYGTGKTAQYLOAQAAHAAGQYADVDFPHKGGAGTEWDAVENPS 124
DB 99 LGEFNQKGTVTKYGTGKTRSQLAQAVTSLKNNGIQYGVVVMHKGADATEMVRAVEVNP 158

QY 125 DRNOEISGTYOIQAWTKDFPGRGNTYSSPKRWVYHFDGVDWDSRKL-SRIYKFRGIGK 183
DB 159 NNEQVTEGYETIAWTRDFPGRGNTYSSPKRWVYHFDGVDWDSRKLNRRIYKFRGHGK 218

QY 184 AWDNEVDTENGNYDLYMADMDHPHEVVTTELKNGKMYNTTINDGFRLDVAKHIKFSF 243
DB 219 AWDNEVDTENGNYDLYMADMDHPHEVVELNNGWYVNTTILGLDGRIDVAKHIKYSF 278

QY 244 FPDMLSVRSOTGKPLFTVGVWYSDINKLHNYITKTGDTMSLDAPLHNKPYTASKGG 303
DB 279 TRDINHVRSGATGKMFVAFEFKNDLGAENLYLQKTNWHSFVDFPLHNLNASKSGG 338

QY 304 AFDMRTLMTNLMDQPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEGYPC 363
DB 339 NYDMENLFNGTVQVRHSHAVTFVDNHSQPEEALESFVFEWFKPLAYALTITREQYPS 398

QY 364 VFYGDYGIPOYNTPSLKSDIPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKPGSG 423
DB 399 VFYGDYGIPTGHPVPMRSKIDPILKARQYAYGKQNDYLDHNIIGWTREGTAPNSG 458

QY 424 LAALITDGPCKGKMYGKQHAGKVFVDLTGNRSDTTVINSQDGEKPYNGGVSVVW 481
DB 459 LATIMSDGAGCKGKMFVGRNKGQVMSDITGNRTGTVTINADGNGFVNGSGVSIWV 516

RESULT 6
ALBSL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus licheniformis
C;Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
C;Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844
R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Udaka, S.
J. Biochem. 98, 1147-1156, 1985
A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
A;Reference number: A91997; MUID:86111694; PMID:2418011
A;Accession: A91997
A;Molecule type: DNA
A;Residues: 1-162,'R',164-512 <YUU>
A;Cross-references: GB:X03236; NID:g939551; PIDN:CAA26981.1; PID:g939552
A;Experimental source: ATCC 27811
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: B24549
A;Molecule type: DNA
A;Residues: 1-338,'G',340-348,'S',350-512 <GRA>
A;Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511
A;Experimental source: NCIB 8061
R;Stephens, M.A.; Orltapp, S.A.; Ollington, J.F.; McConnell, D.J.

J. Bacteriol. 158, 369-372, 1984
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A;Reference number: A91796; MUID:84185455; PMID:6609154
A;Accession: A91796
A;Molecule type: DNA
A;Residues: 1-104 <STP>
A;Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
R;Sibakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase
A;Reference number: A21663; MUID:85076654; PMID:6334606
A;Accession: A21663
A;Molecule type: DNA
A;Residues: 1-3,'H',5-12,'P',14-47,'R',49-61,'V',63,'D',65-67,'VA',70-71,'S',73-80,'D',82;
A;Experimental source: chromosomal DNA of ATCC 14580
A;Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 67
R;Laoid, B.M.; Chambliss, G.H.; McConnell, D.J.
J. Bacteriol. 171, 2435-2442, 1989
A;Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent regulation
A;Reference number: I39773; MUID:89213924; PMID:2540150
A;Accession: I39774
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-29 <LAD>
A;Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction
A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39772
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-32,'I', <JOR>
A;Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499
R;Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
J. Bacteriol. 149, 372-373, 1982
A;Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison with the sequence of the alpha-amylase from Bacillus pasteurii
A;Reference number: A26151; MUID:82098050; PMID:6172418
A;Accession: A26151
A;Molecule type: protein
A;Residues: 30-37,'E',39-41,'X',43-47 <KUH>
R;Machius, M.; Wiegand, G.; Huber, R.
J. Mol. Biol. 246, 545-559, 1995
A;Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.2 angstroms
A;Reference number: S53788; MUID:95182462; PMID:7877175
A;Accession: S53788
A;Molecule type: protein
A;Residues: 'D',220-227 <MAC>
A;Note: sequence represents amino end of an internal fragment created by a single enzymatic cleavage
R;Machius, M.; Wiegand, G.; Huber, R.
submitted to the Brookhaven Protein Data Bank, July 1995
A;Reference number: A65206; PDB:1BPL
A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210;222-511
A;Note: these structural studies suggest 163 is Leu rather than Arg
R;Song, H.K.; Wang, K.Y.; Chang, C.; Suh, S.W.
submitted to the Brookhaven Protein Data Bank, October 1996
A;Reference number: A66860; PDB:1VJS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210;222-511
C;Genetics:
A;Gene: amyL
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide degradation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;207-512/Product: alpha-amylase #status experimental <WAT>
F;227-360/Domain: alpha-amylase core homology <AMY>
F;133,229,264/Binding site: calcium (Asn, Asp, His) #status experimental
F;260,290,357/Active site: Asp, Glu, Asp #status experimental

Query Match 62.9%; Score 1794.5; DB 1; Length 512;
Best Local Similarity 65.0%; Pred. No. 6.7e-122;

Matches 316; Conservative 68; Mismatches 97; Indels 5; Gaps 2;

Qy 1 AAPNGTMMQFPEWYLPDDGTLWTKVANEANLSSLGITLWLPAYKGTSSRDVGYGVY 60
 Db 29 AANLNGTLMQFPEWYMPDNGQHWKRLQNDLSSAYLAEGITAVWIPAYKGTSSQADVGYGAY 88
 Qy 61 DLYDLGFENOGKTVRTKYGTAQYLQATQAAHAAGMOMVADVDPDHKGADGTWDAVE 120
 Db 89 DLYDLGFHQKTVRTKYGTAQYLQATQAAHAAGMOMVADVDPDHKGADGTWDAVE 148
 Qy 121 VNPDRNQEISGTYQIQAWTKFDPFGNGTYSSEFKRWYHFDGVDWDSRKLRIYKPRG 180
 Db 149 VDPADNRNVISGEHLKAWTHFFPGRGSTYSDFKWHYHFDGTDWDSRKLRIYKPRQ- 207
 Qy 181 IGKADWEVDTEGNGYDLYADLMDHPEVVTTELKNGKQVYNTNIDGFRLLDAVKHIK 240
 Db 208 -GKADWEVSENGENYDLYADLMDHPEVVTTELKNGKQVYNTNIDGFRLLDAVKHIK 266
 Qy 241 FSPFPDMLSVRSOTGKPLFTVGEVWSYDINKLHNYITKTDGTMSLDPAFLHNKFTASK 300
 Db 267 FSPFUDWNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNHVSFDPVPLHYQFHAAT 326
 Qy 301 SGGAFDRTLTMTNLMDKQPTLAVTFVNDHDEPGQALQSWVDWPFKPLAYAFILTROEG 360
 Db 327 QGGGYDMKLLNSTVSKHPLKAVTFVNDHDEPGQALQSWVDWPFKPLAYAFILTROEG 386
 Qy 361 YPCVFGDYGI---PQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGT 417
 Db 387 YPQVFGDMYGTGDSQREIPALKHKIEPLKARKQYAYGAQHDYFDHHDIVGWTREGDS 446
 Qy 418 EKPSGGLAALITDGPCKGKMYVQKQAGKVPYDITGNRSSTVINSQGWGEPKNGGSV 477
 Db 447 SVANSGLAALITDGPCKGKMYVQKQAGKVPYDITGNRSSTVINSQGWGEPKNGGSV 506
 Qy 478 SVMVPR 483
 Db 507 SIYQVR 512

RESULT 7
 ALBNS
 N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C;Species: Bacillus amyloliquefaciens
 C;Date: 30-Nov-1980 #sequence revision 30-Jun-1987 #text_change 18-Jun-1999
 C;Accession: A92389; A90307; I39756; I39763; A00843
 R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, I.
 J. Biol. Chem. 258, 1007-1013, 1983
 A;Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr
 A;Reference number: A92389; MUID:83108808; PMID:6185474
 A;Contents: PUB110
 A;Accession: A92389
 A;Molecule type: DNA
 A;Residues: 1-514 <TAX>
 A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA221
 R;Chung, H.S.; Friedberg, F.
 Biochem. J. 185, 387-395, 1980
 A;Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.
 A;Reference number: A90307; MUID:80241725; PMID:6156671
 A;Accession: A90307
 A;Molecule type: protein
 A;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
 R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
 Gene 15, 43-51, 1981
 A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
 A;Reference number: I39756; MUID:82051296; PMID:6170539
 A;Accession: I39756
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-96 <RES>
 A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
 R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karanen, S.
 Gene 59, 161-170, 1987

A;Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by its ow
 A;Reference number: I39763; MUID:88137952; PMID:2830166
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-39 <RES>
 A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
 C;Function:
 A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A;Pathway: glycogen/starch degradation
 C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
 C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F;1-31/Domain: signal sequence #status predicted <SIG>
 F;32-51/Product: alpha-amylase #status predicted <MP1>
 F;229-362/Domain: alpha-amylase core homology <AMY>
 F;133,261/Binding site: calcium (Asn, Asp, His) #status predicted
 F;262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 62.1%; Score 1773.5; DB 1; Length 514;
 Best Local Similarity 65.4%; Pred. No. 2.2e-120;
 Matches 316; Conservative 57; Mismatches 105; Indels 5; Gaps 2;

Qy 5 NGTMMQFPEWYLPDDGTLWTKVANEANLSSLGITLWLPAYKGTSSRDVGYGVYDLYD 64
 Db 33 NGTMMQFPEWYLPDDGTLWTKVANEANLSSLGITLWLPAYKGTSSRDVGYGVYDLYD 92
 Qy 65 LGFENOGKTVRTKYGTAQYLQATQAAHAAGMOMVADVDPDHKGADGTWDAVEVNP 124
 Db 93 LGFENOGKTVRTKYGTAQYLQATQAAHAAGMOMVADVDPDHKGADGTWDAVEVNP 152
 Qy 125 DRNQEISGTYQIQAWTKFDPFGNGTYSSEFKRWYHFDGVDWDSRKLRIYKPRG 184
 Db 153 DRNQEISGTYQIQAWTKFDPFGNGTYSSEFKRWYHFDGVDWDSRKLRIYKPRG 212
 Qy 185 DWEDVDTEGNGYDLYADLMDHPEVVTTELKNGKQVYNTNIDGFRLLDAVKHIK 244
 Db 213 DWEDVDTEGNGYDLYADLMDHPEVVTTELKNGKQVYNTNIDGFRLLDAVKHIK 272
 Qy 245 PDWLSYVRSOTGKPLFTVGEVWSYDINKLHNYITKTDGTMSLDPAFLHNKFTASK 304
 Db 273 PDWLSYVRSOTGKPLFTVGEVWSYDINKLHNYITKTDGTMSLDPAFLHNKFTASK 332
 Qy 305 FDMRTLTMTNLMDKQPTLAVTFVNDHDEPGQALQSWVDWPFKPLAYAFILTROEG 364
 Db 333 FDMRTLTMTNLMDKQPTLAVTFVNDHDEPGQALQSWVDWPFKPLAYAFILTROEG 392
 Qy 365 FYGDMYGTGTSPPK-EIPSLKDNIEPIILKARKEAYGPHQHDYDHPDVIGWTR 420
 Db 393 FYGDMYGTGTSPPK-EIPSLKDNIEPIILKARKEAYGPHQHDYDHPDVIGWTR 451
 Qy 421 GSGLAALITDGPCKGKMYVQKQAGKVPYDITGNRSSTVINSQGWGEPKNGGSV 480
 Db 452 GSGLAALITDGPCKGKMYVQKQAGKVPYDITGNRSSTVINSQGWGEPKNGGSV 511
 Qy 481 VPR 483
 Db 512 VQK 514

RESULT 8
 AH2079
 alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AH2079
 F;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Saemoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.;
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AH2079
 A;Status: preliminary

Db 63 LGFBNQKGTVRTKGYKEDYLAQIAQALKAQGIQPMADVILNHHKAAADHREAFQVIEVDPV 122
Qy 125 DRNQEISGTYQIQAWTKFDPFGRNTYSSFKRWYHFDGVDWDSRKLRIYKFRGIGKA 184
Db 123 DRIVELGEPFTINGTSFTDGRQDTYNGFHHWHYHFTGYDADAKRSKSYLIQGNKG 182
Qy 185 WDNE--VDTEGNYDYIMYADLMDHDEVTTELKNGKQWYVNTNIDGFRDLDAVGHKFS 242
Db 183 WANEELVDNENGNVDYIMYADLDPKPEVIQNIYDMADWFMETTVGAGFRDLDAVGHKIDSF 242
Qy 243 FFPDLVSYSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHKNKPYTASKSG 302
Db 243 FMRNFIRDMKEKYGDDYFVGEFNSKDEANLDYLEKTEEHFDLVDVRLHQNLFASQAG 302
Qy 303 GAFDMRLMTNTLMKQDPTLAVTFVDNHDTPGQALQSWDPWPKPLAYAFILTRQEGYP 362
Db 303 ANYDLRGIFTDSLVELPKDPAVTFVDNHDTRQGALESFVEEWPFPKPAAYALILLRQDGLP 362
Qy 363 CVFYGDYIGIP-QYNIPSLKSKIDPLLIARDYAYGTHQHYLDHSDIIGWTREGTEKPG 421
Db 363 CVFYGDYIGISGQYAOQDFKELDLRLAIRKDLAYGEQNDYFDHANGIGWVRSQAENQ-- 420
Qy 422 SGLAALITDGGSKWYVQKQAGKVFYDLTGNRSDTVTINSQWGEKFKVNGSVSVWV 481
Db 421 SPIAVLINSQENSKSMFVGOEWNTQTFVDLLGSHQGVITDEEGYCGFPVARSARSVW- 479
Qy 482 PRKTTVSTI 490
Db 480 ---AVNTI 484

RESULT 11

alpha-amylase (EC 3.2.1.1) - Bacillus circulans

C;Species: Bacillus circulans
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999

A;Accession: S15713

R;Marcel, T.

submitted to the EMBL Data Library, May 1991

A;Reference number: S15713

A;Accession: S15713

A;Molecule type: DNA

A;Residues: 1-493 <MAR>

A;Cross-references: EMBL:X60779; NID:G39411; PIDN:CAA43194.1; PID:G39412

C;Genetics:

A;Gene: amyE

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

P;200-333/Domain: alpha-amylase core homology <AMY>

Query Match 44.8%; Score 1278.5; DB 2; Length 493;
Best Local Similarity 48.5%; Pred. No. 1.2e-84;
Matches 232; Conservative 84; Mismatches 159; Indels 3; Gaps 2;

Qy 5 NGTMQYFEWYLPDDGTLWTKVANEANLSSIGITALMLPPAYKGTSRSDVGYGYDLYD 64
Db 4 NHTMQYFEWLAADGDHMKLAEMAPELKAGIDTVWVPVTKAVSAEDTGYGYDLYD 63
Qy 65 LGFBNQKGTVRTKGYKQYLAQIAQAAHAGQVYADVVDHKGADGTEWDAVEVNP 124
Db 64 LGFBNQKGTVRTKGYKQYLAQIAQAAHAGQVYADVVDHKGADGTEWDAVEVNP 123
Qy 125 DRNQEISGTYQIQAWTKFDPFGRNTYSSFKRWYHFDGVDWDSRKLRIYKFRGIGKA 184
Db 124 DRKEISPEPFEIGTWKTFPGRGDYSSFKWNSHFNGTDFDAREERTGVFRIAGENKK 183
Qy 185 WDNEVDTEGNYDYIMYADLMDHDEVTTELKNGKQWYVNTNIDGFRDLDAVGHKFSFF 244
Db 184 WNEVDTEGNYDYIMYADLMDHDEVTTELKNGKQWYVNTNIDGFRDLDAVGHKFSFF 243

Qy 245 PDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHKNKPYTASKSGGA 304
Db 244 KEFAAEMIRKRGQDFYIVGEFNSNLDACREFLDTYDQIDLDLFDVSLHYKLHEASLGRD 303
Qy 305 FDMRTLTMTNTLMKQDPTLAVTFVDNHDTPGQALQSWDPWPKPLAYAFILTRQEGYPCV 364
Db 304 FDLKSKFPDDLTVOTHPHATVTFVDNHDSPQHEALESWIGDWFKPSAYALTLLRRDGYPV 363
Qy 365 FYGDYIGI--PQYNIPSLKSKIDPLLIARDYAYGTHQHYLDHSDIIGWTREGTEKPGS 422
Db 364 FYGDYIGIGGPE-PVDGKKEILDILLSARCNAKYGQEDYFDHANTIGWVRRGVETEGS 422
Qy 423 GLAALITDGGSKWYVQKQAGKVFYDLTGNRSDTVTINSQWGEKFKVNGSVSVW 480
Db 423 GCAVWISNGDDGKRMFGEHRAGEVWVDLTKSCDDQITIEEDGWATFHVCGGGSVW 480

RESULT 12

C86781

alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

A;Accession: C86781

R;Bolooin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: C86781

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-491 <STO>

A;Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: amyL

C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 43.1%; Score 1229; DB 2; Length 491;

Best Local Similarity 47.5%; Pred. No. 4.3e-81;

Matches 231; Conservative 73; Mismatches 176; Indels 6; Gaps 5;

Qy 7 TMMQYFEWYLPDDGTLWTKVANEANLSSIGITALMLPPAYKGTSRSDVGYGYDLYD 65

Db 3 TILQAFEWYLPDSQHNWNIKENIPDLGKLGFGSLWLPAPKASGVEDYGYGYDLYD 62

Qy 66 GEFNOKGTVRTKGYKQYLAQIAQAAHAGQVYADVVDHKGADGTEWDAVEVNP 125

Db 63 GEFNOKGTVRTKGYKQYLAQIAQAAHAGQVYADVVDHKGADGTEWDAVEVNP 121

Qy 126 RN-QEISGTYQIQAWTKFDPFGRNTYSSFKRWYHFDGVDWDSRKLRIYKFRGIGKA 184

Db 122 NHLHNIENNTVETWTKFTFPGRQGYDNYITWHTFTGIDYDERKQKELEPE--GHE 179

Qy 185 WDNEVDTEGNYDYIMYADLMDHDEVTTELKNGKQWYVNTNIDGFRDLDAVGHKFSFF 244

Db 180 WDNEVDTEGNYDYIMYADLMDHDEVTTELKNGKQWYVNTNIDGFRDLDAVGHKFSFF 239

Qy 245 PDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGTMSLFDAPLHKNKPYTASKSGGA 304

Db 240 DKWLEQRAKQJDRKLFIVGETWSDDLKLEYLEQSSDRQLQFVPLHFNKKEASSTNGE 299

Qy 305 FDMRTLTMTNTLMKQDPTLAVTFVDNHDTPGQALQSWDPWPKPLAYAFILTRQEGYPCV 364

Db 300 FDMRTLTMTNTLMKQDPTLAVTFVDNHDTPGQALQSWDPWPKPLAYAFILTRQEGYPCV 359

Qy 365 FYGDYIGI--PQYNIPSLKSKIDPLLIARDYAYGTHQHYLDHSDIIGWTREGTEKPGSGL 424

Db 360 FWGDLGYPGSHVNPVGNLRTMLAKRDSFELRENDYFDHPDIIIGTWNILKIDNKEYGL 419

Qy 425 AALITDGGSKWYVQKQAGKVFYDLTGNRSDTVTINSQWGEKFKVNGSVSVWVPRK 484

Db 420 SCILTNKNGGSKYIMIDKAYAGKYYIDLFGRHEIPTLDQNGGAFFVNDGSGSVWVD-K 478

QY 485 TTVSTI 490
 Db 479 EIVSKI 484

RESULT 13

B45738
 alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
 N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Salmonella typhimurium
 C/Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
 C/Accession: B45738

R/Raba, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R. M.

J. Bacteriol. 174, 6644-6652, 1992

A/Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.

A/Reference number: A45738; MUID:93015717; PMID:1400215

A/Accession: B45738

A/Molecule type: DNA

A/Residues: 1-494 <RAH>

A/Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045

C/Genetics:

A/Gene: amyA

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C/Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

F/202-335/Domain: alpha-amylase core homology <AMY>

F/239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.0%; Score 1112.5; DB 1; Length 494;
 Best Local Similarity 44.0%; Pred. No. 1.1e-72;
 Matches 216; Conservative 83; Mismatches 175; Indels 17; Gaps 5;

QY 5 NGTMMQYFEWYLPDGGTLWTKVANEANNLSLIGITALWLPAYKGTSSR-DVGVGYVDLY 63

Db 3 NPTLLQYFHWYYPDGGKLSLAERADGLNDGINWVWLPACKGASGVSGYDYDLF 62

QY 64 DLGEFNOKGTVTKYGTAKYQLOAQAAHAAGMOYADVVDVHHKGGADGTWDAVEVNP 123

Db 63 DLGEFDQKGTATYKDGKRLQLTAIDALKKNIAVLDDVVVNHKMGADKERIRVQRVNO 122

QY 124 SDRNQEISGYTQIAWTKFDPFGRGNTYSSFKRWVHFDGVDWDSRKLSTRYKPRG--I 181

Db 123 DRTQIDDDNIIECEGWTRYTFPARAGQYSNFIWDYHCFSGIDHIENPDDEGIFKIVNDYT 182

QY 182 GKAWDEVDTEGNGYDYLMTADLMDHPEVVTTELKNWGWYVNTTNDGPRLDVAKHIF 241

Db 183 GDGWNQVDDEMGNFYLMGENIDFRNHAITEIKYWARVWMEQTHCDGFRLDVAKHIFA 242

QY 242 SFPPDWLSYVRSGTKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASKS 301

Db 243 WFKYEWIEHVQVAPKPLFVAEYWSHSEVDKLTQYIDQVKGKTLFDPALQMKFHEASRQ 302

QY 302 GGAFDMRTLMTLMKDOPTLATVFDNHDTEPGQALOSWVDWPFKPLAYAFILTRQEGY 361

Db 303 GAEDMRHIFTGLVEADPFHATVLANHDTQLQALEAPVEPWFKPLAYALILLRENGV 362

QY 362 PCVFYGDYGYIP-----QYNIPSLKSIDPLLIARRDYAYGTOHLDHSDIIG 410

Db 363 PSVFYDLYGASYEDSGENGETCRVDMPIV-NQLDRLLARQRFAGIQTLPFDHPNCIA 421

QY 411 WTEGGTEKPGSGLAALITDGGSKMWYGVKGHAGKVFDLTGNRSDDTVTINSQGWGF 470

Db 422 FSRSGTEENP--GCVVVLSNGDDGKTLILGDNVANKTWDRDFSGNRDEYVVTNDQGEATF 479

QY 471 KVNNGSVSVWV 481

Db 480 FCNAGSVSVWV 490

RESULT 14

AD0751

cytoplasmic alpha-amylase [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C/Species: Salmonella enterica subsp. enterica serovar Typhi
 A/Note: this species has also been called Salmonella typhi
 C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C/Accession: AD0751

R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AD0751

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-494 <PAR>

A/Cross-references: GB:AL513382; PIDN:CAD05711.1; PID:g16503204; GSPDB:GN00176

C/Genetics:

A/Gene: STY2171

C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 38.6%; Score 1101.5; DB 2; Length 494;

Best Local Similarity 44.0%; Pred. No. 7e-72;

Matches 216; Conservative 82; Mismatches 176; Indels 17; Gaps 5;

QY 5 NGTMMQYFEWYLPDGGTLWTKVANEANNLSLIGITALWLPAYKGTSSR-DVGVGYVDLY 63

Db 3 NPTLLQYFHWYYPDGGKLSLAERADGLNDGINWVWLPACKGASGVSGYDYDLF 62

QY 64 DLGEFNOKGTVTKYGTAKYQLOAQAAHAAGMOYADVVDVHHKGGADGTWDAVEVNP 123

Db 63 DLGEFDQKGTATYKDGKRLQLTAIDALKKNIAVLDDVVVNHKMGADKERIRVQRVNO 122

QY 124 SDRNQEISGYTQIAWTKFDPFGRGNTYSSFKRWVHFDGVDWDSRKLSTRYKPRG--I 181

Db 123 DRTQIDDDNIIECEGWTRYTFPARAGQYSNFIWDYHCFSGIDHIENPDDEGIFKIVNDYT 182

QY 182 GKAWDEVDTEGNGYDYLMTADLMDHPEVVTTELKNWGWYVNTTNDGPRLDVAKHIF 241

Db 183 GDGWNQVDDEMGNFYLMGENIDFRNHAITEIKYWARVWMEQTHCDGFRLDVAKHIFA 242

QY 242 SFPPDWLSYVRSGTKPLFTVGEYSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASKS 301

Db 243 WFKYEWIEHVQVAPKPLFVAEYWSHSEVDKLTQYIDQADGKTLFDPALQMKFHEASRQ 302

QY 302 GGAFDMRTLMTLMKDOPTLATVFDNHDTEPGQALOSWVDWPFKPLAYAFILTRQEGY 361

Db 303 GAEDMRHIFTGLVEADPFHATVLANHDTQLQALEAPVEPWFKPLAYALILLRENGV 362

QY 362 PCVFYGDYGYIP-----QYNIPSLKSIDPLLIARRDYAYGTOHLDHSDIIG 410

Db 363 PSVFYDLYGASYEDSGENGETCRVDMPIV-NQLDRLLARQRFAGIQTLPFDHPNCIA 421

QY 411 WTEGGTEKPGSGLAALITDGGSKMWYGVKGHAGKVFDLTGNRSDDTVTINSQGWGF 470

Db 422 FSRSGTEENP--GCVVVLSNGDDGKTLILGDNVANKTWDRDFLGNRSEHVVTNDQGEATF 479

QY 471 KVNNGSVSVWV 481

Db 480 FCNAGSVSVWV 490

RESULT 15

AD3038

Alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C/Accession: AD3038

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I

ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-495 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:gl7742354; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: amyA
A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

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Query Match      37.8%; Score 1078.5; DB 2; Length 495;
Best Local Similarity 44.4%; Pred. No. 3.2e-70;
Matches 218; Conservative 75; Mismatches 179; Indels 19; Gaps 6;

QY  7 TMMQYFEWYLPDDGTLMTKVAANEANLSSLGITALLWLPAYKGTSSRS-DVGYGVYDLYDL 65
Db  :||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
5  TLLQFFHMYYPDGGKLMSEVAEKAESLAKMGITDVLPPAYKGAAGGYSVGYDLYDLFDL 64

QY  66 GEFNOKGTVRTKYGTQAQYLQAIQAAHAAGMQVYADVVDHKGAGDGTGEWDAVEVNPSP 125
Db  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65  GEFQKGTVAATKYGDRAALEHAGKILKONGIRVHDVVLNKHMGADKEKEKVRVRVPDD 124

QY  126 RNOEISGTYQIAWTKFDFPGRGNTYSFQKRWYHFDGVDWDESRKLSRIYKF---RGIG 182
Db  :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
125  RTDIDDEDFPALAYTRTFPGRNKGKSKFIWDLKCFSGVDHIEEPTEDGIFRLVNEYGDG 184

QY  183 KANDWEVDTEGNDYDLYMYADLMDHPEVVTTELKNWKGWYVNTNIDGFRDLDAVKHIKFS 242
Db  :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
185  E-WNEEYDQENGNDYLDGADVEFRNRAVYBELKYGWRWLSQVQVDGFRLDAAKHIPAW 243

QY  243 FEPDMLSVRSQCKPLFTVGEYWSYDINKLHNVTITKDTGMSLFDAPLHNKFYTASKSG 302
Db  ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
244  FFRDWGHRRTVDPDLFVVAEYHWPDLKLSYELVLDKQLMDFVALHSHFHDASKQG 303

QY  303 GAFDMRTLMTLTKMQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEGYP 362
Db  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
304  GDFDMRSIFDGLSVSAVDPDHAVTLVDNHDTPQLSLEAPVEPFPKPLAYAILLREEGVP 363

QY  363 CVFYGDYYGIP-----QYNIPSLKSKIDPLLIARDYAYGTQHDYLDHSDIIGW 411
Db  |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
364  CVFYPDLFGTSYDTGNDGNEYKIDIPAIEC-LPKLIEARSRFANGPQTDFDDASCIAF 422

QY  412 TREGTEKPGSGLAALITDGPCKWYVGVKQHAGKVPYDLTGNRSDTVTINSQGWGEFK 471
Db  ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
423  IRHGTADAP--GCVVVMNGEPGKQADLGPFRAGSVWRDPLGHRHEHITLDESCKGTFP 480

QY  472 VNGGSVSVWVP 482
Db  |||||
481  TNGGSVSVWVP 491
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Search completed: October 7, 2004, 00:20:43
Job time : 16.8068 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 9.03245 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-6
Perfect score: 2854
Sequence: 1 AAFPNGTMMQYFEWYLPDDG.....TRPWTGEFVWTSPLVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2787	97.7	549	1 AMY_BACST	P06279 bacillus sp
2	1874.5	65.7	518	1 AMT6_BACS7	P19571 bacillus sp
3	1797.5	63.0	512	1 AMY_BACLI	P06278 bacillus li
4	1773.5	62.1	514	1 AMY_BACAM	P00692 bacillus am
5	1110.5	38.9	494	1 AMY2_SALTY	P26613 salmonella
6	1074.5	37.6	495	1 AMY2_ECOLI	P26612 escherichia
7	313	11.0	713	1 CDGT_BACSP	P30921 bacillus sp
8	307	10.8	1196	1 AMYB_PAEPO	P21543 paenibacill
9	302.5	10.6	440	1 AM3A_ORYSA	P27932 oryza sativ
10	302	10.6	713	1 CDGT_BACS8	P17692 bacillus sp
11	300	10.5	713	1 CDGT_BACCI	P43379 bacillus ci
12	286.5	10.0	712	1 CDGT_BACB3	P09121 bacillus sp
13	286	10.0	718	1 CDGT_BACLI	P14014 bacillus li
14	284.5	10.0	713	1 CDGT_BACSO	P05618 bacillus sp
15	283	9.9	421	1 AMYA_VIGMU	P17859 vigna mungo
16	282	9.9	718	1 CDGT_BACSS	P31747 bacillus sp
17	280	9.8	413	1 AMY3_WHEAT	P08117 triticum ae
18	278	9.7	718	1 CDGT_BACCI	P30920 bacillus ci
19	275.5	9.7	564	1 AMY1_SCHPO	Q9Y789 schizosacch
20	274.5	9.6	438	1 AM3B_ORYSA	P27937 oryza sativ
21	274.5	9.6	528	1 AMY_BACCI	P08137 bacillus ci
22	273	9.6	710	1 CDGT_THETU	P26827 thermoanaer
23	272.5	9.5	428	1 AMY1_ORYSA	P17654 oryza sativ
24	271.5	9.5	437	1 AM3C_ORYSA	P27939 oryza sativ
25	268.5	9.4	438	1 AMY1_HORVU	P00693 hordeum vul
26	268	9.4	711	1 CDGT_BACST	P31797 bacillus st
27	266.5	9.3	429	1 AMY6_HORVU	P04750 hordeum vul
28	266	9.3	435	1 AM3D_ORYSA	P27933 oryza sativ
29	262.5	9.2	427	1 AMY2_HORVU	P04063 hordeum vul
30	262	9.2	703	1 CDGT_BACS2	P31746 bacillus sp
31	258.5	9.1	368	1 AMY3_HORVU	P04747 hordeum vul
32	257.5	9.0	437	1 AM3E_ORYSA	P27934 oryza sativ
33	253.5	8.9	494	1 AMY1_SACFI	P21567 saccharomyc

RESULT 1				
AMY_BACST	AMY_BACST	STANDARD;	PRT;	549 AA.
ID	AC	F06279; Q45519;		
DT	DT	01-JAN-1988 (Rel. 06, Created)		
DT	DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan		
DE	DE	glucanohydrolase).		
GN	GN	AMYS.		
OS	OS	Bacillus stearothermophilus.		
OC	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.		
OX	OX	NCBI_TaxID=1422;		
RN	RN	[1]		
RP	RP	SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.		
RX	RX	MEDLINE=85234394; PubMed=3924897;		
RA	RA	Nakajima R., Imanaka T., Aiba S.;		
RT	RT	"Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase		
RT	RT	gene."		
RL	RL	J. Bacteriol. 163:401-406(1985).		

34	249	8.7	443	1	AM2A_ORYSA	P27935 oryza sativ
35	248	8.7	498	1	AMYA_ASPAW	Q02905 aspergillus
36	248	8.7	499	1	AMYB_ASPAW	Q02906 aspergillus
37	247	8.7	499	1	AMY_ASPSH	P30292 aspergillus
38	245	8.6	499	1	AMYA_ASPOR	P10529 aspergillus
39	244	8.5	919	1	AMY_STRLI	Q05884 streptomyce
40	242	8.5	445	1	AMC3_ORYSA	P27941 oryza sativ
41	238.5	8.4	498	1	AMY3_DICTH	P14899 dictyoglomu
42	236	8.1	581	1	AMY1_SCHPO	Q09840 schizosacch
43	230.5	8.1	713	1	CDG2_PAEPA	P31835 paenibacill
44	224.5	7.9	704	1	CDGT_BACOH	P27036 bacillus oh
45	224	7.8	624	1	AMY1_LIPKO	Q01117 lipomyces k

ALIGNMENTS

RL J. Biol. Chem. 265:15481-15488 (1990).

RP [9] MUTAGENESIS OF ALA-238.

RC STRAIN=ATCC 6598;

RX MEDLINE=96367070; PubMed=8771184;

RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;

RT "Hyperthermostable mutants of *Bacillus licheniformis* alpha-amylase:

RT multiple amino acid replacements and molecular modelling.";

RL Protein Eng. 8:1029-1037 (1995).

RN [10]

RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;

RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359

RP AND GLU-365.

RC STRAIN=ATCC 6598;

RX MEDLINE=20425100; PubMed=10966804;

RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;

RT "Probing structural determinants specifying high thermostability in

RT *Bacillus licheniformis* alpha-amylase.";

RL J. Mol. Biol. 301:1041-1057 (2000).

RN [11]

RP MUTAGENESIS OF GLN-293 AND ASN-294.

RC STRAIN=ATCC 6598;

RX MEDLINE=22622182; PubMed=12736372;

RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,

RA Gaillardin C.;

RT "Hyperthermostabilization of *Bacillus licheniformis* alpha-amylase and

RT modulation of its stability over a 50 degrees C temperature range.";

RL Protein Eng. 16:287-293 (2003).

RN [12]

RP MUTAGENESIS OF TRP-292 AND VAL-315.

RC STRAIN=ATCC 27811;

RX MEDLINE=22797417; PubMed=12915728;

RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;

RT "Alpha-amylase from *Bacillus licheniformis* mutants near to the

RT catalytic site: effects on hydrolytic and transglycosylation

RT activity";

RL Protein Eng. 16:505-514 (2003).

RN [13]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RC STRAIN=ATCC 27811;

RX MEDLINE=95182462; PubMed=7877175;

RA Machius M., Wiegand G., Huber R.;

RT "Crystal structure of calcium-depleted *Bacillus licheniformis* alpha-

RT amylase at 2.2-A resolution.";

RL J. Mol. Biol. 246:545-559 (1995).

RN [14]

RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RC MEDLINE=98212915; PubMed=9551551;

RA Machius M., Declerck N., Huber R., Wiegand G.;

RT "Activation of *Bacillus licheniformis* alpha-amylase through a

RT disorder-->order transition of the substrate-binding site mediated

RT by a calcium-sodium-calcium metal triad.";

RL Structure 6:281-292 (1998).

RN [15]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 330-512.

RC MEDLINE=20384196; PubMed=10924103;

RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,

RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;

RT "Structural analysis of a chimeric bacterial alpha-amylase.

RT High-resolution analysis of native and ligand complexes.";

RL Biochemistry 39:9099-9107 (2000).

RN [16]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT

RC STRAIN=ATCC 6598;

RX MEDLINE=22538505; PubMed=12540849;

RA Machius M., Declerck N., Huber R., Wiegand G.;

RT "Kinetic stabilization of *Bacillus licheniformis* alpha-amylase through

RT introduction of hydrophobic residues at the surface.";

RL J. Biol. Chem. 278:11546-11553 (2003).

CC -/- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

CC linkages in oligosaccharides and polysaccharides.

CC -/- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC

CC -/- SUBUNIT: Monomer.

CC -/- BIOTECHNOLOGY: Used in the food industry for high temperature

CC liquefaction of starch-containing mashes and in the detergent

CC industry to remove starch. Sold under the name Termamyl by

CC Novozymes.

CC -/- MISCELLANEOUS: Able to work at relatively high (alkaline) pH

CC values (up to pH 11) and at high temperatures (up to 100 degrees

CC Celsius).

CC -/- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

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CC or send an email to license@isb-sib.ch).

CC

CC EMBL; X03236; CAA36981.1; -

CC EMBL; M38570; AAA22226.1; -

CC EMBL; M13256; AAA22240.1; -

CC EMBL; K01984; AAA22193.1; -

CC EMBL; A5438149; AAO26743.1; -

CC EMBL; M26412; AAA22237.1; -

CC EMBL; A17930; CAA01355.1; -

CC PIR; A91997; ALBSL.

CC PDB; 1BLI; 23-MAR-99.

CC PDB; 1BPL; 17-AUG-96.

CC PDB; 1E3X; 21-JUN-01.

CC PDB; 1E3Z; 24-JUN-03.

CC PDB; 1E40; 24-JUN-03.

CC PDB; 1E43; 21-JUN-01.

CC PDB; 1O80; 03-APR-03.

CC PDB; 1VJS; 12-MAR-97.

CC InterPro; IPR006589; Alp.amyl_cat_sub.

CC InterPro; IPR006047; Alpha.amyl_cat.

CC InterPro; IPR006046; Glyco.hydro_13.

CC Pfam; PF00128; alpha-amylase; 1.

CC PRINTS; PR00110; ALPHAAMYLASE.

CC SMART; SM00642; Amy; 1.

CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;

CC Signal; 3D-structure.

CC SIGNAL 1 29

CC CHAIN 30 512 ALPHA-AMYLASE.

CC ACT_SITE 260 260

CC ACT_SITE 264 264

CC ACT_SITE 357 357

CC METAL 133 133

CC METAL 190 190

CC METAL 210 210 CALCIUM 1.

CC METAL 212 212 CALCIUM 2 AND SODIUM.

CC METAL 223 223 CALCIUM 2 AND SODIUM.

CC METAL 229 229 CALCIUM 1 AND SODIUM.

CC METAL 231 231 CALCIUM 1 AND SODIUM.

CC METAL 233 233 CALCIUM 2.

CC

CC Query Match 63.0%; Score 1797.5; DB 1; Length 512;

CC Best Local Similarity 65.0%; Pred No. 2e-120;

CC Matches 316; Conservative 69; Mismatches 96; Indels 5; Gaps 2;

CC

CC 1. AAPFNGTMMQYFEWYLPDDGTLTKVANEANNSLSGITLWLPAYKGTGRSDYGYVY 60

CC 29 AANLNGTLNQYFEWYMPNDGQHWKRLQND SAYLAEHGITA VMPYKGTQADYGYGAY 88

CC

CC 61 DLYDLGEFNGKGTVRTKTYQAYLQAOIAAHAGMQYADVVDHKKGAGTEWDAVE 120

CC 89 DLYDLGEFHQGTVRTKTYGTELQSAIKSLHSRDINVGVDVWVNHKGGADATEDVTA 148

CC 121 VNPSDRNCEISGTQIOAWTKFPDPRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180

CC 149 VDPADNRNVIAGEHRKAWTHFFPGRGSTYSDFKWHWHYFDGTDWDSRKLRIYKQ- 207

CC 181 IGKAWDEVDTENGNYDYLMYADLMDHPFVVTELKNWKYVNTNTDGRFLDAVKHK 240

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Db 208 -GRADWEVSENGNDYLAIDYDHPVAAEIKRWGTWYANELQDGRFLDAVKHIK 266
Qy 241 FSFPDRLSVRSOTGKPLFTVGEYMSYDKLNHNYITKTDGMSLFDAPLHKNFYTASK 300
Db 267 FSLRDWNVHREKTKGEMTVAEYQNDLGALENLYNKTNFHSVDFVPLHVQFHAAS 326
Qy 301 SGGAFTMTLNTLTKMDQPTLAVTFVDNHDTPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 327 QGGGDMRKLNTSVSKPLKAVTFVDNHDTPGQSLSTVOTWFKPLAYAFILTRQEG 386
Qy 361 YPCVFVGDYGI---PQYNIPSLKSKTDPLLIARDVAYGTQHDYLDHSDIIGWTRGGT 417
Db 387 YPQVFYGDYGTGDSQREIPALKHLEPILKARKQAYGAQHDYDFDHDIVGWTRGDS 446
Qy 418 EKPGSGLAALITDGPCKGKMYVGVKQHAGKVFYDLTGNRSDTVTINSKGWGEFVNGGVS 477
Db 447 SVANSGLAALITDGPCKAKMYGVQRQAGETWHDITGNRSEPVVINSEGWGEFVNGGVS 506
Qy 478 SVMVPR 483
Db 507 SIVQR 512

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RESULT 4

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AMY_BACAM
ID _BACAM STANDARD; PRT; 514 AA.
AC P00692;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
  glucanohydrolase).
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Pattersson R.F., Kalkkinen N., Palva I., Soederlund H.,
  Kaeerlaeinen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
  deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RN SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
  amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RN SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Pattersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
  Soederlund H., Takkinen K., Kaeerlaeinen L.;
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
  region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RN SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karanen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
  its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkmenburg J.P., Bisgaard-Frantzen H.,
  Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.

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RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
  linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
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  or send an email to license@isb-sib.ch).
EMBL; J01542; AAA22191.1; -
EMBL; V00092; CAA23430.1; -
EMBL; A20154; CAA01489.1; -
EMBL; M18424; AAA22192.1; -
PIR; A92389; ALBSN.
PDB; 1E3X; 21-JUN-01.
PDB; 1E3Z; 24-JUN-03.
PDB; 1E40; 24-JUN-03.
PDB; 1E43; 21-JUN-01.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; P00110; ALPHAAMYLASE.
SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
  Signal; 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 514
FT ACT_SITE 262 262
FT ACT_SITE 292 292
FT ACT_SITE 359 359
FT METAL 133 133
FT METAL 190 190
FT METAL 212 212
FT METAL 214 214
FT METAL 225 225
FT METAL 231 231
FT METAL 233 233
FT METAL 235 235
FT METAL 266 266
FT METAL 331 331
FT METAL 438 438
FT METAL 461 461
FT CONFLICT 54 54
FT CONFLICT 64 64
FT CONFLICT 79 79
FT CONFLICT 84 84
SQ SEQUENCE 514 AA; 58403 MW; 3DE66B3FB5CCDE7E CRC64;
  62.1k; Score 1773.5; DB 1; Length 514;
  Best Local Similarity 65.4k; Pred. No. 1e-118;
  Matches 316; Conservative 57; Mismatches 105; Indels 5; Gaps 2;

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Qy 5 NGTMMQYFEWYLPDDGTLTKVANEANLISLIGITALWLPAYKGTSRSDVGYGYDLYD 64
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Db 33 NGTLQMIFEWYTPNDGQHKRLQNDAEHLSDIGITAVWIPAYKGLSQSDNGYGYDLYD 92
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 65 LGFEENQKGTVRTKYTKAQYLQAIQAHAAGMGOYADVDFDHKGAGDGTWDAVENPS 124
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 LGFEQKGTVRTKYTKSELQDAIGSLHSRNVQYGVGVNHNKAGADATEDVTAVEVNP 152
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 125 DRNOEISGTQIQAWTKFDPFGRTNTVSSFKRWYHFDGVWDERSKLSRIYKRGIGKA 184
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 NRNOETSEYQIKAWTDFFPFGRTNTVSDFKWHYHFDGADWDSRKISRIYKRGIGKA 212
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 185 WDNEVDTEGNYDYLMYADLMDHPPEVVTTELKNGKGYVNTTNDGRLDVAVKHKESFF 244
Db 213 WDWESSENGYDYLMYADLMDHPPEVVTTELKNGKGYVNTTNDGRLDVAVKHKESFF 272
QY 245 PDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKDTGWSLDPAPLHNFYTASKSGGA 304
Db 273 RDWQAVRQATGKEMFTVAETWQNNAGKLENLTKTSFNQSVFVDPVPHFNQAASSGGG 332
QY 305 FDMRTLMTNTLMKDQPTLAVFDVNDHDTPEQALQSWVDWPFKPLAYAFILTRQEGYPCV 364
Db 333 YDMERLLDGTWVSRHPEKAVTFVENHDTQPGSLESSTVQWFKPLAYAFILTRQEGYPCV 392
QY 365 FYGDIYGI-----POYNPSLKSXKIDPLLIARDYVAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 393 FYGDMYTKGTSPK-EIPSLKDNIEPILKARKEYAYGPHDYIDHPDVIWGTREGDSAA 451
QY 421 GSGLAALITDPPGSGKMYVKGQHAGKVFYDLTGNSRDTVTINSDDGGEFKVNGSGSVW 480
Db 452 KSGLAALITDPPGSGKMYAGLKNAGETWYDITGNRSDDTVKIGSDGGEFHVNDGVSIIY 511
QY 481 VPR 483
Db 512 VQK 514

RESULT 5
AMY2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase).
GN AMYA OR STM1963.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=JW1103;
RC MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=U72 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT L72.";
RL Nature 413:852-856(2001).
RN [3]
RN SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=JW1103;
RC MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [4]
RN SEQUENCE OF 476-494 FROM N.A.
RC MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIb, including a

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RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
CC EMBL; L01643; AAA27110.1; -.
CC EMBL; AB008787; AAL20875.1; -.
CC EMBL; M85241; AAA27079.1; -.
CC EMBL; L13280; AAA71970.1; -.
CC PIR; B45738; B45738.
CC HSSP; P06278; IVJS.
CC StyGene; SGI0011; amyA.
CC InterPro; IPR006589; Alp_amyl_cat_sub.
CC InterPro; IPR006047; Alpha_amyl_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC SMART; SM00642; Aamy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5E47C CRC64;
Query Match 38.9%; Score 1110.5; DB 1; Length 494;
Best Local Similarity 44.0%; Pred. No. 1.2e-71; Indels 17; Gaps 5;
Matches 216; Conservative 82; Mismatches 176;
QY 5 NGTMQYFEWYLPDQGLTWKTVKANEANLSSIGITALLWLPAYKGTSSRS-DVGYGYDYLY 63
Db 3 NPTLLQYFHWYVDPGCKLWSELAEADGLNDIGINWVLPACKGASGGYVGYDYLYDLF 62
QY 64 DLGEFNQKGTIVTKYGTAKYQLOAQAAHAGMQVYADVVDHKGADGTEWDAVEVNP 123
Db 63 DLGEFDQKGTIATKYGDKRQLLTALDALKNNIAVLDDVYVNHKMGADKERRIVQVNVQ 122
QY 124 SRNQEISGTYOIOAWTKFDFPGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKPRG--I 181
Db 123 DRTQIDDDNIICEGWTRITFFPARAGYISNF1WDHCFSGIDHIEPNDEGIFKIVNDYT 182
QY 182 GKAWDEVDTEGNYDYLMYADLMDHPPEVVTTELKNGKGYVNTTNDGRLDVAVKHKIF 241
Db 183 GDGNDQVDDENGNFDYLMGENIDFRNHAETEEIKYWARVMEQTHCDGRLDVAVKHIA 242
QY 242 SFFPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKDTGWSLDPAPLHNFYTASKS 301
Db 243 WYKWEIWHVQAVAPKPLFIVAETWYSHVEDLQTVTDQVDGKTMLFDPALQMKFHEASRQ 302
QY 302 GGAFTDMRTLMTNTLMKDQPTLAVFDVNDHDTPEQALQSWVDWPFKPLAYAFILTRQEGV 361
Db 303 GAEDMRHIFTGLTLEADPFHATVILVANHDTPQLQLEAPVFWFKPLAYALLIRENGV 362
QY 362 PCVFYGDYGYGIP-----QYNIPSLKSIDPLLIARDYVAYGTQHDYLDHSDIIG 410
Db 363 PSVFYFDLYGASVEDSGENGETCRVDMPIV-NQDLRLILARQRFAGHIGITLFFDHNCIA 421
QY 411 WTREGGTEKPGSGLAALITDPPGSGKMYVKGQHAGKVFYDLTGNSRDTVTINSDDGGEF 470

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Db 422 FSRSGTEENP--GCVVVLSNGDGEKTLILLGDNVANKYKTRDPLGNRDEYVVVTTNDQGEATF 479
Qy 471 KVGSGSVVWV 481
Db 480 FCNAGSVVWV 490

RESULT 6
ID AMY2 ECOLI STANDARD; PRT; 495 AA.
AC P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL1.
RX MEDLINE=33015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayaashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIb, including a
RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; L01642; AAA23810.1; --
CC EMBL; AE000285; AAC74994.1; --
CC EMBL; D90833; BAA15755.1; --
CC EMBL; M85240; --; NOT ANNOTATED_CDS.
CC EMBL; L13279; AAA82575.1; --
CC PIR; D64956; A45738.
CC HSP; P06278; 1VJS
CC EcoGene; EG11387; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Complete proteome.
CC ACT_SITE 235 235 BY SIMILARITY.
CC ACT_SITE 265 265 BY SIMILARITY.
CC ACT_SITE 332 332 BY SIMILARITY.
CC METAL 104 104 CALCIUM (BY SIMILARITY).
CC METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC CONFLICT 19 20 KL -> SS (IN REF. 1).
CC CONFLICT 109 109 A -> V (IN REF. 1).
CC CONFLICT 149 149 Q -> E (IN REF. 1).
CC CONFLICT 234 234 L -> I (IN REF. 1).
CC SEQUENCE 495 AA; 56639 MW; 26AFP6797DDA54D6 CRC64;
Qy 5 NGTMMQYFEWYLPDDGTLTKVANEANLSSGLTALWLPAYKGTSSR-DVGVGVVDLY 63
Db 3 NPTLLQCFHWYYPGGKLPALRADGDFNDIGINWVLPAYKAGSGGVSGVSYDLF 62
Qy 64 DLGEFNGKGVTRTKYKQAOYLQAIQAAHAGQVYADVDFDKHGGADGTWVDVAVNP 123
Db 63 DLGEFDGKGSIPYKYGKQAQLLAIDALKENDIAVLDDVVNKHGDAKEAIRVQRVA 122
Qy 124 SDRNQEISGTYQIQAWTKFPDPCRGNTYSSFKRWYHFDGVWDSDSKLSRIYKFRG--I 181
Db 123 DDRQTQIDEEIIECEGWTRYTFPARAGQYSQFIWDFKCFSGIDHIENPDEGIFKIVNDYT 182
Qy 182 GKAWDEVDTEGNYDYLAVADLMDHPVETELKWKGVVNTTNDGRLDVAKHKP 241
Db 183 GEGNDQVDDDELGNFDYLMGENIDFRNHAETEEIKYWARWMEQTQCDGFLDVAKHPPA 242
Qy 242 SFPDNLVSVRSQTKPLFTVGEVSYDINKLHNYIKTKDQTSLSLFDAPLHNKFTASKS 301
Db 243 WFKWEIHEVQEVAPKPLFVAEYWSHEVDKLTQYIDQVEGKTMFLDAPLQMKHEASRM 302
Qy 302 GGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPQALQSWVDPMFKPLAVAFILTROEGY 361
Db 303 GRDYDMTQIIFTGLVEADPFHVLTVANHDTPQLQALEAPVEPWFKPLAVAILRENGV 362
Qy 362 PCVPYGYGYIPQVNIIPS-----LKSKDPLLIARDVAYGTQHYLDHSDLIIGW 411
Db 363 PSVFYPLDYGAEHVDVGGGQGTYPIDMPIIEQLDELILARQRFAGHYQTLLFFDHPNCIAF 422
Qy 412 TREGGTEKPGSLAALITDGGGSKWYVKGQAGKVFYDLTGNRSSTVITNSDGMGEFK 471
Db 423 SRSGTDEFF--GCVVVMSNGDDGKEKTHLGENYGNKTRDPLGNRQERVVTDENGAEATFF 480

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Query Match 37.6%; Score 1074.5; DB 1; Length 495;
Best Local Similarity 42.9%; Pred. No. 4.4e-69;
Matches 210; Conservative 83; Mismatches 182; Indels 15; Gaps 4;

QY 472 VNGGSVSVWV 481
Db 481 CNGGSVSVWV 490

RESULT 7

CDGT_BACSP STANDARD; PRT; 713 AA.

AC P30921;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGT.

OS Bacillus sp. (strain 17-1).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.

RA MEDLINE=90257592; PubMed=2534600;

RX Kaneko T., Song K.B., Hamamoto T., Kudo T., Horikoshi K.;

RT "Construction of a chimeric series of Bacillus cyclomaltoedextrin

RT glucanotransferases and analysis of the thermal stabilities and pH

RT optima of the enzymes";

RL J. Gen. Microbiol. 135:3447-3457(1989).

CC -! CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation

CC of a 1,4-alpha-D-glucosidic bond.

CC -! COFACTOR: Binds 2 calcium ions per subunit (By similarity).

CC -! SUBUNIT: Monomer.

CC -! MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE

CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND

CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER

CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN

CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE

CC MALTOLOGISACCHARIDE PRODUCED.

CC -! SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----M28053; AAA22310.1; --

DR HSP; P43379; 1CDG.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006048; Alpha_amy1_C.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR002044; CBD_4.

DR InterPro; IPR006046; Glyco_hydro_13.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR002909; IPT_TIG.

DR Pfam; PF00129; alpha-amy1ase; 1.

DR Pfam; PF02806; alpha-amy1ase_C; 1.

DR Pfam; PF00686; CBM_20; 1.

DR Pfam; PF01833; TIG; 1.

DR PRINTS; PR00110; ALPHAAMYLASE.

DR ProDom; PD001568; CBD_4; 1.

DR SMART; SM00642; Amy; 1.

DR SMART; SM00632; Amy; 1.

KW transferase; Glycosyltransferase; Calcium-binding; Signal.

FT SIGNAL 1 27

FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.

FT DOMAIN 28 165 A1.

FT DOMAIN 166 229 B.

FT DOMAIN 230 433 A2.

FT DOMAIN 434 522 C.

FT DOMAIN 523 609 D.

FT DOMAIN 610 713 E.

FT ACT_SITE 256 256 BY SIMILARITY.

FT ACT_SITE	284	284	BY SIMILARITY.
FT ACT_SITE	355	355	BY SIMILARITY.
FT METAL	54	54	CALCIUM 2 (BY SIMILARITY).
FT METAL	56	56	CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
			SIMILARITY).
FT METAL	59	59	CALCIUM 2 (BY SIMILARITY).
FT METAL	60	60	CALCIUM 2 (BY SIMILARITY).
FT METAL	78	78	CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
			SIMILARITY).
FT METAL	80	80	CALCIUM 2 (BY SIMILARITY).
FT METAL	166	166	CALCIUM 1 (BY SIMILARITY).
FT METAL	217	217	CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
			SIMILARITY).
FT METAL	226	226	CALCIUM 1 (BY SIMILARITY).
FT METAL	260	260	CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
			SIMILARITY).
FT DISULFID	70	77	BY SIMILARITY.
SQ SEQUENCE	713 AA;	77389 MW;	D13AEF6C507FF45E CRC64;

Query Match 11.0%; Score 313; DB 1; Length 713;

Best Local Similarity 24.7%; Pred.No. 8.6e-15;

Matches 135; Conservative 82; Mismatches 188; Indels 142; Gaps 29;

QY 19	DGTL-----	WTKVANEANN--	SSLGITLWLP--	---AYKTSRSDVGYGYDL 62
Db 67	DGTCNLRLYCGDMQGIINKINDGYLTGVTAIWISQPVENIYVINGVNNYAHG 126			
QY 63	YDLGEFNQKGVTRTKYTKAQVLAQAAHAGMOYADVDFHKGGA--	DGTWVDVAVE 120		
Db 127	YWARDPK---	TNPAYGTIADFQNLTAHAKNIKVIIDFAFNHTSPASLDQPSFAENGK 183		
QY 121	VNPSRDNQISGTQIQOAMTKDFPGRGNTYSFKRWYHFDGVDWDESKLSRIYKPRG 180			
Db 184	LYNNGRDE--	GGY-----	TNDTNLF----	HHNGGTDFS----- 211
QY 181	IGKAMDWEVDTEGNYDYLM--	YADLMDHPEVVTBLKNWGWYVNTNIDGFRDLDAVRHI 239		
Db 212	-----	TTENGIYKNLYDLADLNHNNSVTDTYLDKAIKWLD--	LGIDGIRMDAVKHM 261	
QY 240	KFSFPDMLSVRSQTGKPLFTVGEYWSVDINKL--	HNYYTKDTGTMSLFDAPLHNKPYT 297		
Db 262	PFGWOKSFMVNNY--	KPVFTFGE--	WFLGVNEVSAENHKFANVSGMSLLDPRFAQKVRQ 318	
QY 298	ASK--	SGGAFFDMRTLMTNTL-----	MKDQPTLAVTFVDNHDTE----	PGQALQSWDVPWFK 347
Db 319	VFKDNTDNMYGLKSMLEGSATDYAQMEDQ----	VTFINHDMERFHNSANRKLQEQ----	371	
QY 348	PLAYAFILTRQEGYPCVGYGYGIPQY-----	NIPS-----	LKSKIDPL 387	
Db 372	--ALAFTLT--	SRGVPAI----	YGTQYMSGNDPDNRARIPSFSTTTTAYQVSKKLAPL 424	
QY 388	LIARRDYAGTQHDYLDHSDIIGWTREGGTE-----	KPGSLAALITDGPSSKW 437		
Db 425	RKSNPAIAYGTQERWINNDVLIYERKFNNVAVTAVNRNNTSASITGLVTSLPAGS--	482		
QY 438	MYVGKHAGKVPYDLTGN--	RSDDVTINSDDGME--	FKVNGGSVSW--	VPRTTSTIAR- 492
Db 483	-----	YTDVLGLLNGNLTGSGGSASITLAAAGTAVWQYTTAVTAPTIGHV 531		
QY 493	-PITTRP 498			
Db 532	GPMMAKP 538			

RESULT 8

AMVB_PAEPO STANDARD; PRT; 1196 AA.
ID AMVB_PAEPO
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amy1ase precursor [includes: Beta-amy1ase (EC 3.2.1.2);
DE Alpha-amy1ase (EC 3.2.1.1)].


```
QY 461 TNSDGM-----GEF-----KVGSGSVSWV-PRKTTVST 489
DB 1141 VFNNWNSQRTTIGNFDNLNGRLTNQLSNDVSQINNGSIITVLAPKEVKVFT 1195

RESULT 9
AM3A_ORYSA
ID AM3A_ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -!- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
CC -!- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; X56336; CAA39776.1; -.
DR PIR; S14958; S14958.
DR HSSP; P04063; IAVA.
DR Gramene; P27932; -.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 440
FT ACT_SITE 207 207 ALPHA-AMYLASE ISOZYME 3A.
FT ACT_SITE 315 315 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT METAL 145 145 CALCIUM 1 (BY SIMILARITY).
FT METAL 155 155 CALCIUM 2 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 3 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 3 (BY SIMILARITY).
FT METAL 170 170 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 171 171 SIMILARITY).
FT METAL 170 170 CALCIUM 1 (BY SIMILARITY).
FT METAL 171 171 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 171 171 SIMILARITY).

FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 176 176 SIMILARITY).
SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 10.6%; Score 302.5; DB 1; Length 440;
Best Local Similarity 28.4%; Pred. No. 2.7e-14;
Matches 117; Conservative 47; Mismatches 147; Indels 101; Gaps 21;

QY 8 MMQYFEW-YLPDDGTLTKVANEANLSSLGITALLMPPAYKGTSTSDVGYVDLYDLG 66
DB 31 LFGFNWDSWKQGGWYNMLKQDQVGIASAGVTHVWLPPTH--SVSPQGYMPGRLYDLN 88
QY 67 EFNQKGTVRTKYGTAKYLAQIAAHAAAGVQVADVVDHKGAGDGTWVDAVEVNPSTR 126
DB 89 -----ASKYGTAKELSLIAAFKAGIKCVADIVNHRCAD----- 125
QY 127 NQISGTYQIAWTKFDFPGRNTYSSFKRWYHFDGVWDSESKLSRYKFR-GIGKAW 185
DB 126 -KDRGVYCI-----FKGGGPR-----GCLDWGSPSMICDDDTQYSDGTGHR- 165
QY 186 DWEVDTEGNYDYLWYADLMDHDPVVTTELKNWGWVNTTINIDGERLDAVKHKESFPP 245
DB 166 -----DT---GADFAAAPDIDHLNPLVQRELSDWLRRLRDVGDGWRDLFAKGYSAVA- 217
QY 246 DWLSYVRSQTKPLFTVGEYW---SYD-----INKLHNYITKTDGTMSLPDAF 290
DB 218 --RTYV--QNAKPSFVVAISWNSLSYDGGKPAANDGQORQELVNWVWQVGGPATADF 273
QY 291 LHNKFTASKSGGAFDMRTMTNTLMKD-----QPTLAVTFVDNHDTPGQALQSW 341
DB 274 TKGILQSAVQ-GELWFRMD-----KDGKAPGMIGWPEKAVTFVDNHD--GSTQRMW 323
QY 342 VDPWPKP-LAYAFILTRQEGYCVFYGVYGPQYPOYNIPSLKSKIDPLLIARR 392
DB 324 PFPDSKVILGYAYILT-HPGVPCIFYDQVF---DMN---LKQEINALAATRK 368

RESULT 10
CDGT_BACS8
ID CDGT_BACS8 STANDARD; PRT; 713 AA.
AC P17692;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltoextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting
DE amylase).
OS Bacillus sp. (strain B1018).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1417;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
RX MEDLINE=90147765; PubMed=1689153;
RA Itokor P., Tsukagoshi N., Uda S.;
RT "Nucleotide sequence of the raw-starch-digesting amylase gene from
RT Bacillus sp. B1018 and its strong homology to the cyclodextrin
RT glucanotransferase genes.";
RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
CC -!- FUNCTION: This endo-type adsorbable amylase is capable to
CC digest raw starch.
CC -!- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -!- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC EMBL; M33302; AAA22239.1; -.
CC EMBL; D90112; BAA14140.1; -.
DR PIR; S09196; S09196.
DR HSP; P43379; ICDG.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR InterPro; IPR006048; Alpha_aml_C.
DR InterPro; IPR006047; Alpha_aml_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002909; IFT_TIG.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG_1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
KW Transferase; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNAL 1 27
FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT ACT_SITE 256 256 BY SIMILARITY.
FT ACT_SITE 284 284 BY SIMILARITY.
FT ACT_SITE 355 355 BY SIMILARITY.
FT METAL 54 54 CALCIUM 1 (BY SIMILARITY).
FT METAL 56 56 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 59 59 SIMILARITY).
FT METAL 59 59 CALCIUM 1 (BY SIMILARITY).
FT METAL 60 60 CALCIUM 1 (BY SIMILARITY).
FT METAL 80 80 CALCIUM 1 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 2 (BY SIMILARITY).
FT METAL 217 217 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 226 226 SIMILARITY).
FT METAL 260 260 CALCIUM 2 (BY SIMILARITY).
FT METAL 260 260 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 713 713 AA; 77420 MW; 85FB616DA687B888 CRC64;
SQ SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;

Query Match 10.6%; Score 302; DB 1; Length 713;
Best Local Similarity 24.7%; Pred. No. 5.2e-14;
Matches 136; Conservative 80; Mismatches 205; Indels 130; Gaps 29;

QY 2 APFNGTWQVFEWYLPDGTGLTKVANEANN--LSSLGITALLWLP--AYKGTSSDV 55
DB 64 AAFDGTCTN--LRLYCGD---WQGIINKINDGYLTGMVTAIWISQPVENIYSIINSGV 119
QY 56 GYGVYDLYDLGEFNQKGTVRTKYTKAQYLQAIQAHAAGQVYADVVFHKGADGTW 115
DB 120 NNTAYHGYWARDFKK---TPAYGTIADFQNLIAAHAHAKIKVIIDFAPNHTSPASSDQP 176
QY 116 VDAVEVNPDRNQBEISGTQIQIQAQWTKDFPGRGNWYSSFKRWTHFDGVWDSEKLSRI 175
DB 177 SFAENGRLYD--NGTLGGY-----TNDTQNLF-----HHNGGTDPS----- 211
QY 176 YKFRGICKANDWEVDTEGNYDLYLWYADLMDHDEEVTE--LKNWGWYNTNTNIDGRL 233
DB 212 -----TTENGYYKNL--YDLADLNHNNSDSDVYLKDAIKRWLD--LGIDGIRM 255
QY 234 DAVKHIFSPDPDLSVRSQTKPLFTVGYWYSYDINKL--HNYITKTDGMSLDFAPL 291
DB 256 DAVKHPFGQKSPMAAVNNY--KPVTFGE--WFLGVNEVGPENKHNANESGMSLLDFR 312
QY 292 HNKFYTA--SKSGGAFDMRTLMNTNL-----MKDQPLAVTFVNDHPTQCALQSWVDP 344
DB 313 AQKRVQVRFDNTDMYGLKALEGSAADYAQVDDQ-----VTFIDHMERPHAGNANRKK 368
QY 345 WFKDLAVAFILTRREGVPCVGYDYGIPQY-----NTPSLKS-----KI 384
DB 369 LEQALAFILAR---VPAI-----YGTQYMSGGTDPDNRRARIPSFSTTAYQVQKL 421

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QY 385 DPLLIARRDYAYGTQHDYLDHSDIIGWTRGGT-----EKPGSLAALITDPCG 433
DB 422 APLRKNPATAYGSTQERWINNDVLIYERKFSNVAVVAVNRNLNAPAS--ISGLVTSLPQ 480
QY 434 GSKWMYVGKQHACKVFDLTGN--RSDVTIINDG--WGEFKVNGSVSW--VPRKTTVST 489
DB 481 GS-----YNDVLGGLLNGNTLVGSGGAASFTLAAGGTAVWQYTAATATPT 527
QY 490 IAR--PITTRP 498
DB 528 IGHVGPMMAKP 538

RESULT 11
CDGU_BACCI
ID_CDGU_BACCI STANDARD; PRT; 713 AA.
AC P43379;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
OS Bacillus circulans
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 28-37, AND X-RAY CRYSTALLOGRAPHY (2.0
RP ANGSTROMS).
RC STRAIN=251;
RX MEDLINE=94149761; PubMed=8107143;
RA Lawson C.H., van Montfort R., Strokopytov B., Rozeboom H.J.,
RA Kalk K.H., de Vries G.E., Penninga D., Dijkhuizen L., Dijkstra B.W.;
RT "Nucleotide sequence and X-ray structure of cyclodextrin
RT glycosyltransferase from Bacillus circulans strain 251 in a maltose-
RT dependent crystal form.";
RL J. Mol. Biol. 236:590-600(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC STRAIN=251;
RX MEDLINE=96094317; PubMed=7493956;
RA Knegtel R.M.A., Strokopytov B., Penninga D., Faber O.G.,
RA Rozeboom H.J., Kalk K.H., Dijkhuizen L., Dijkstra B.W.;
RT "Crystallographic studies of the interaction of cyclodextrin
RT glycosyltransferase from Bacillus circulans strain 251 with natural
RT substrates and products.";
RL J. Biol. Chem. 270:29256-29264(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=97115811; PubMed=8955113;
RA Penninga D., van der Veen B.A., Knegtel R.M.A., van Hijum S.A.F.T.,
RA Rozeboom H.J., Kalk K.H., Dijkstra B.W., Dijkhuizen L.;
RT "The raw starch binding domain of cyclodextrin glycosyltransferase
RT from Bacillus circulans strain 251";
RL J. Biol. Chem. 271:32777-32784(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH INHIBITOR.
RC STRAIN=251;
RX MEDLINE=96264806; PubMed=8672460;
RA Strokopytov B., Knegtel R.M.A., Penninga D., Rozeboom H.J., Kalk K.H.,
RA Dijkhuizen L., Dijkstra B.W.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT maltotriose inhibitor at 2.6-A resolution. Implications for product
RT specificity.";
RL Biochemistry 35:4241-4249(1996).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- DOMAIN: May consist of two protein domains: the one in the amino-
CC terminal side cleaves the alpha-1,4-glucosidic bond in starch, and
CC the other in the C-terminal side catalyzes other activities,
CC including the reconstitution of an alpha-1,4-glucosidic linkage
CC for cyclizing the maltooligosaccharide produced.

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```
Db 138 AYGTMDPKNLDTAHAENIKVIIDFAPNHTSPASSDDPSFAENGRLYD-NGNLLGGY-- 194
Qy 137 QAWTKFDFPGRGNTYSSSKFWYHDFDGVWDDESRLKLSRIYKFRGIGKAWDEVDTEGNY 196
Db 195 -----TNDTONLF-----HHYGGTDFS-----TIENGIIY 218
Qy 197 DYLW-YADLMDHPEVTELRKNGWKYVNTTNDIGFRLDAVKHKFSPFPDWLSYVSQT 255
Db 219 KNLVDLADLNHNSVDVYLKDAIKWLD-LGVDIRVDAVKHMPFGWKQSFMTINNY- 276
Qy 256 GKPLFTVGEYSYDINKL-----HNYITKDTGMLFADPLHNKPYTA--SKSGGAFDMRT 309
Db 277 -KPVNFGE-WFLGVNEISPEYHOFANESG--MSLLDFPFAQKARQVFRDNTDNNYGLKA 332
Qy 310 LMTWT-----LWKDQPTLAVTFVDNHDTEPCQALQSWDPWFKPLAVAFILTRQEGYPCV 364
Db 333 MLEGEVDYAVQNDQ-----VTFIDHDMERHTSNG--DRKLEQALAFILT-SRGVPAI 385
Qy 365 FYGDIYGIPOY-----NIPSLKS-----KIDPLLIARDYAYGTOHDYLD 404
Db 386 ---YIGSEQVMSGNDPNRARIPISTTTTAYQVIQKLAFLKSNPAIAYGSTQERWI 441
Qy 405 HSDLIIGTREGGT-----EKPGSLAALITDGPQSGKMYGVKQHAGKVFYDLT 453
Db 442 NNDVILIERKFGNNVAVVAINRNMNTPAS-ITGLVTSLPQGS-----YNDVL 487
Qy 454 GN--RSDVTITNSDG-WGEFKVNGSVSVMPVKTTVST 489
Db 488 GGILNGNTLVGAGGAASNTFLAPGCTAVW--QYTTDAT 524

RESULT 13
CDGT_BACLI
ID _CDGT_BACLI STANDARD; PRT; 718 AA.
AC P14014.1
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGTA
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90174931; PubMed=2137908;
RA Hill D.E., Aldape R., Rozzell J.D.;
RT "Nucleotide sequence of a cyclodextrin glucosyltransferase gene,
RL cgtA, from Bacillus licheniformis.";
RL Nucleic Acids Res. 18:199-199(1990).
CC -I- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.
CC -I- COPACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -I- SUBUNIT: Monomer.
CC -I- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15752; CAA33763.1; -.
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DR PIR; S15920; ALBSMX.
DR HSPP; P30920; ICGT.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD 4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PD00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD 4; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C; 1.
DR TRANSF; Glycosyltransferase; Calcium-binding; Signal.
KW TRANSF; Glycosyltransferase; Calcium-binding; Signal.
FT SIGNAL 1 34 BY SIMILARITY.
FT CHAIN 35 718 A1.
FT DOMAIN 35 172 A1.
FT DOMAIN 173 236 B.
FT DOMAIN 237 440 A2.
FT DOMAIN 441 528 C.
FT DOMAIN 529 614 D.
FT DOMAIN 615 718 E.
FT ACT_SITE 258 258 BY SIMILARITY.
FT ACT_SITE 291 291 BY SIMILARITY.
FT ACT_SITE 362 362 BY SIMILARITY.
FT METAL 61 61 CALCIUM 2 (BY SIMILARITY).
FT METAL 63 63 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 66 66 CALCIUM 2 (BY SIMILARITY).
FT METAL 67 67 CALCIUM 2 (BY SIMILARITY).
FT METAL 85 85 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 87 87 CALCIUM 2 (BY SIMILARITY).
FT METAL 173 173 CALCIUM 1 (BY SIMILARITY).
FT METAL 224 224 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 233 233 CALCIUM 1 (BY SIMILARITY).
FT METAL 267 267 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT DISULFID 77 84 BY SIMILARITY.
FT SEQUENCE 718 AA; 78002 MW; B3CDE14A81D5DC4E CRC64;

Query Match 10.0%; Score 286; DB 1; Length 718;
Best Local Similarity 23.1%; Pred. No. 7,2e-13;
Matches 138; Conservative 78; Mismatches 196; Indels 186; Gaps 30;

Qy 2 APFNGTMMQYFEWYLPDDGTLWTQVANEANN--LSSLGITLWLP--YKG- 49
Db 71 AAFDGTCSN-LKLYCGGD---WQGLVKNINDNYFSDGLGVTALWISQPVENIPATINYSGV 126
Qy 50 TSSRSDVGYGVVDLGLGDFNQGKGVTRTKYKAQYLOIAHAAAGMOMVYADVDFHKG 109
Db 127 TNYAYGVYWARDFKKINPY-----FGTWDFQNLVTTAAHAKGIKIIDFAPNHTSP 177
Qy 110 ADGTWDAVEVNPDSRDNQEIISGTYQIAWTKDFPGRGNTYSSFKWRYHDPGVWDDES 169
Db 178 AMETDTSFAENGKLYDNGNLVGG-----YTNDTNGY-----FHNGGSDFS-- 218
Qy 170 RKLRIYKFRGIGKAWDEVDTEGNYDYLW-YADLMDHPEVTELRKNGWKYVNTTNI 228
Db 219 -----TLENGIYKNLYDLADLNHNSNTIDTYFQDAIKLWLD-MGV 257
Qy 229 DGFRLDAVKHKFSPFPDWLSYVSQTKPLFTVGEYSYDINKLHNYITKDTGT----- 283
Db 258 DGIIRDVAVKHMPQGWKQNMSSIVAH--KPVFTGGEW-----LGSAAPADNATDFANE 309
Qy 284 --MSL-----FADAPLHNKEYTASKSGGAFDMETLMTNTL-----MKDQPTLAVTFVDNHD 332
Db 310 SGMSLLDPRFNSAVRNFRDNTSNMYALD--SMLTAAADYNQNDQ-----VTFIDNHDM 363
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RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
RL Plant Physiol. 103:1459-1459(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COPACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X53049; CAA37217.1; -;
DR EMBL; X73301; CAA51734.1; -;
DR PIR; S10514; S10514.
DR HSP; P04063; LAVA.
DR InterPro; IPR006589; Alp_aml cat sub.
DR InterPro; IPR006047; Alpha_aml cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT SIGNAL 1 23 PROBABLE.
FT CHAIN 24 421 ALPHA-AMYLASE.
FT ACT SITE 201 201 BY SIMILARITY.
FT ACT SITE 309 309 BY SIMILARITY.
FT METAL 113 113 CALCIUM 1 (BY SIMILARITY).
FT METAL 130 130 CALCIUM 2 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT METAL 170 170 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;

Query Match 9.9%; Score 283; DB 1; Length 421;
Best Local Similarity 26.3%; Pred. No. 6.1e-13;
Matches 103; Conservative 48; Mismatches 142; Indels 98; Gaps 17;

QY 8 MMOVFEWLPDDGTLWTKVANEANNLSLGLTALWLPAYKTSRSDVGVGYDLYDLGE 67
DB 26 LFQGFNWESEKKGWYNSLKNIPDLNAGITHVWLP--PSQSVSEGYLPGRLYDL- 82
QY 68 FNQKGTVRTYKTYQAOYLAQAAHAGMOYADVDFDHKGG--ADGTWWDVADEVNPSD 125
DB 83 -----ASKYGSKNELSLIAAFHEKIGKCLADIVINHRHTAERKDGRIYCIIEGGTPD 135
QY 126 RNEISCTYQIQAWTKFPGFRGNTYSSFKRWYTHFDGVWDSEKLSRIYKFRGIGKAW 185
DB 136 SRQDWGSPFCRDDTAYS-DGTGNDS-----GEGY 165
QY 186 DWEVDYENGVDYLYADLMDH--PEVVTLEKNWKKWYNTTNDIGFRLDAVKHKFSP 243
DB 166 D-----AAPDIDLHNPQVRELSEMMNLKTEIGFDGWRDFVK-----GY 206
QY 244 FPWLSYVRSGTKPLFTVGEYW---SY-----DINK--LHNYITKDTGMSLFD 288
DB 207 APS-ISKIYNEQTKPDFAVGEKWDISYGDCKPNYNQDSHRGALVNWVESAGGAIATFD 265
QY 289 -----APLHNKFTASKSGGAFDMRTLMNTLMKDOPTLATVFDVNNHDTPEGQALQS 340
DB 266 FTTKGILQAQVQGLWRLIDPNG-----KPPGMIGVKPENAVTFIDNHD--GSTQRL 316

Qy 341 WVDPMFKPL-AYAFILTRQSGYPCVFGDY 370
Db 317 WPPPSDKVMQGYAYILT-HPGTSPSIFYDHEF 346

Search completed: October 7, 2004, 00:13:20
Job time : 11.0324 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 49.3774 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-6
Perfect score: 2854
Sequence: 1 AAPFNGTMQYFEWYLPDDG.....TRPWTGEFVWTEPRILVAMP 515

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2840	99.5	549	2	Q31193
2	2818	98.7	549	2	Q9Kw16
3	2658	93.1	521	2	P71034
4	2404	84.2	613	2	Q59222
5	1910.5	66.9	516	2	Q82839
6	1841.5	64.5	533	2	Q9A054
7	1837.5	64.4	519	2	Q9RQ78
8	1829.5	64.1	513	16	Q81AS4
9	1827.5	64.0	513	16	Q81XJ4
10	1700	59.6	507	16	Q87HG6
11	1618	56.7	501	2	Q31148
12	1345.5	47.1	492	16	Q8YU21
13	1322.5	46.3	481	16	Q891P1
14	1315	46.1	484	16	Q97Q49
15	1311	45.9	484	16	Q8DPC8
16	1296	45.4	488	16	Q8E0M2

17	1295	45.4	488	16	Q8E696	Q8E696 streptococc
18	1278.5	44.8	493	2	Q03657	Q03657 bacillus c1
19	1268	44.4	486	16	Q8DT08	Q8DT08 streptococc
20	1260	44.1	484	2	O50583	O50583 streptococc
21	1244	43.6	485	2	O53786	O53786 streptococc
22	1237	43.3	486	2	O68875	O68875 streptococc
23	1229	43.1	491	16	Q9CG59	Q9CG59 lactococcu
24	1101.5	38.6	494	16	Q8Z5S5	Q8Z5S5 salmonella
25	1078.5	37.8	506	16	Q8U916	Q8U916 agrobacteri
26	1077.5	37.8	495	16	Q8FGL8	Q8FGL8 escherichia
27	1074.5	37.6	495	16	Q8XBB6	Q8XBB6 escherichia
28	1066.5	37.4	495	16	Q7UAB0	Q7UAB0 shigella fl
29	1064.5	37.3	495	16	Q83R40	Q83R40 shigella fl
30	967	33.9	529	3	Q877B1	Q877B1 aspergillus
31	486	17.0	461	1	Q8NKR5	Q8NKR5 thermococcu
32	483.5	16.9	461	1	Q8NKR4	Q8NKR4 thermococcu
33	482	16.9	469	1	O50200	O50200 thermococcu
34	481	16.9	461	1	O33476	O33476 pyrococcus
35	475	16.6	460	1	O08452	O08452 pyrococcus
36	475	16.6	473	17	Q8U319	Q8U319 pyrococcus
37	474	16.6	460	1	Q9P9L0	Q9P9L0 pyrococcus
38	472.5	16.6	432	14	Q8JZK3	Q8JZK3 uncultured
39	468.5	16.4	457	1	O93647	O93647 thermococcu
40	326.5	11.4	482	2	Q60051	Q60051 thermoactin
41	317	11.1	906	10	Q8LQK4	Q8LQK4 oryza sativ
42	307.5	10.8	423	10	Q8LBS5	Q8LBS5 arabidopsis
43	307.5	10.8	423	10	Q8VZ56	Q8VZ56 arabidopsis
44	307	10.8	826	10	Q9CAR6	Q9CAR6 arabidopsis
45	307	10.8	887	10	Q94A41	Q94A41 arabidopsis

ALIGNMENTS

RESULT 1

O31193 ID O31193 PRELIMINARY; PRT; 549 AA.
AC O31193;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Alpha amylase.
GN AMI.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF032864; AAB86961.1; -
DR PIR; A54541; A54541.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SMO0642; Amy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;

Query March 99.5%; Score 2840; DB 2; Length 549;
Best Local Similarity 99.6%; Pred. No. 2.4e-186;
Matches 513; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AAPFNGTMQYFEWYLPDDGTLWTKVANEANNSLGLTALWLPAYKTSRSDVGIVY 60
Db 35 AAPFNGTMQYFEWYLPDDGTLWTKVANEANNSLGLTALWLPAYKTSRSDVGIVY 94
Qy 61 DLYDLGFEFNQKGTVRTKYTKAQYLAQIAHAAGMQYADVDFDHKGADGTETWDAVE 120

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Db 95 DLYDLGEFNGKGTVRTKYTKAQYLOAIQAAHAAGMOVYADVDFDHKGAGDTEWDAVE 154
QY 121 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
Db 155 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 214
QY 181 IGKAWDEVDTEGNGYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240
Db 215 IGKAWDEVDTEGNGYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 274
QY 241 FSFPDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 300
Db 275 FSFPDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 334
QY 301 SGGAFDMRTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394
QY 361 YPCVFGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGGTEK 420
Db 395 YPCVFGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGGTEK 454
QY 421 GSGLAALITDGPGGSKWYVKGQHAGKVFDLTGNSRDTVTINSDDGGEFKVNGGSVSW 480
Db 455 GSGLAALITDGPGGSKWYVKGQHAGKVFDLTGNSRDTVTINSDDGGEFKVNGGSVSW 514
QY 481 VPRKTTVSTIARPTTRPWTGFEVVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPTTRPWTGFEVVRWTEPRLVAMP 549

RESULT 2
Q9KMY6
ID Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC Q9KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR FBL; A54541; A54541.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycoelidase; Hydrolase.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRC64;

Query Match 98.7%; Score 2818; DB 2; Length 549;
Best Local Similarity 99.0%; Pred. No. 7.7e-185;
Matches 510; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEWYLPDDGTLTWKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 60
Db 35 AAPFNGTMQYFEWYLPDDGTLTWKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 94
QY 61 DLYDLGEFNGKGTVRTKYTKAQYLOAIQAAHAAGMOVYADVDFDHKGAGDTEWDAVE 120
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Db 95 DLYDLGEFNGKGTVRTKYTKAQYLOAIQAAHAAGMOVYADVDFDHKGAGDTEWDAVE 154
QY 121 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
Db 155 VNFSDRNOEISGTYQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 214
QY 181 IGKAWDEVDTEGNGYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 240
Db 215 IGKAWDEVDTEGNGYDLYMYADLMDHPEVVTTELKNWGWYVNTNIDGFRDLDAVKHIK 274
QY 241 FSFPDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 300
Db 275 FSFPDWLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTGTMSLFADPLHNKFTYASK 334
QY 301 SGGAFDMRTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDVPWFKPLAYAFILTRQEG 394
QY 361 YPCVFGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGGTEK 420
Db 395 YPCVFGDYGYGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGGTEK 454
QY 421 GSGLAALITDGPGGSKWYVKGQHAGKVFDLTGNSRDTVTINSDDGGEFKVNGGSVSW 480
Db 455 GSGLAALITDGPGGSKWYVKGQHAGKVFDLTGNSRDTVTITSDDGGEFKVNGGSVSW 514
QY 481 VPRKTTVSTIARPTTRPWTGFEVVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPTTRPWTGFEVVRWTEPRLVAMP 549

RESULT 3
P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC P71034;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RL "Molecular cloning and expression of the gene encoding for thermostable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

Query Match 93.1%; Score 2658; DB 2; Length 521;
Best Local Similarity 99.2%; Pred. No. 6.6e-174;
Matches 480; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAPFNGTMQYFEWYLPDDGTLTWKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 60
Db 35 AAPFNGTMQYFEWYLPDDGTLTWKVANEANNLSLIGITALMLPPAYKGTSRSDVGYGY 94
QY 61 DLYDLGEFNGKGTVRTKYTKAQYLOAIQAAHAAGMOVYADVDFDHKGAGDTEWDAVE 120
|||||
```


Db 37 NGTMMQYFEWHLPNDCNHNRLRDDAANLKSIGITAVWIPPAWKGTSQNDVGVYDAYDLYD 96
QY 65 LGFENQKGTVRTKYGTKAQYLOAQAHAAAGQVYADVDFDHKGADGTEWDAVEVNPS 124
Db 97 LGFENQKGTVRTKYGTRSQLQCAVTSLSKNNGIQVYGVGVMMHKGAGDGTWMAVAVNRS 156
QY 125 DRNQEISCTYIOIQAWTKEFDFGRGNTYSSPKRWYHFDGVWDSDSRKL-SRIYKFRGIGK 183
Db 157 NRNOEISGEYIEATWKEFDFGRGNTSNFKNRWYHFDGTDQDSQRLQNKIYKFRGTGK 216
QY 184 AWDDEVDPENGNDYLMYADLMDHPPEVVTYELKKNWQKYYVNTTIDGFRDLDAVXHKIPSF 243
Db 217 AWDDEVDIENGNDYLMYADLMDHPPEVVTYELKKNWQKYYVNTTIDGFRDLDAVXHKIYS 276
QY 244 FPDMLSVYRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASKSGG 303
Db 277 TRDWLTHVRNTTGKMPFAVAFKNDLAAIENYLNKTSWNHVSFDPVPLHNYLNASNGG 336
QY 304 AFDMRLTMTNLMKDOPTLATVFDNHDTEPGQALQSVDWDFKPLAYAFILTRQEGYPC 363
Db 337 YFDMRNLINGSVQKHPHIAVTFVDNHDSPQGEALSFVQSWFKPLAYALILTRQEGYPS 396
QY 364 VFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKPGSG 423
Db 397 VFYGDYGIPTGHPVPSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGSSHPSNG 456
QY 424 LAALITDPGSGKMYGKQHAGKVFYDLTGNRSDDTVTINSDDGMBFKVNGSGSVWV 481
Db 457 LATIMSDPGGKMYGKQHAGKVFYDLTGNRSDDTVTINSDDGMBFKVNGSGSVWV 514

RESULT 6
Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
KSM B-404".
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CBCEGDA19C7DDE CRC64;

Query Match 64.5%; Score 1841.5; DB 2; Length 533;
Best Local Similarity 65.8%; Pred. No. 5.9e-118;
Matches 317; Conservative 70; Mismatches 92; Indels 3; Gaps 1;
QY 5 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLPYPAYKTSRSDVGVYDLYD 64
Db 52 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLPYPAYKTSRSDVGVYDLYD 111
QY 65 LGFENQKGTVRTKYGTKAQYLOAQAHAAAGQVYADVDFDHKGADGTEWDAVEVNPS 124
Db 112 LGFENQKGTVRTKYGTKAQYLOAQAHAAAGQVYADVDFDHKGADGTEWDAVEVNPS 171
QY 125 DRNQEISCTYIOIQAWTKEFDFGRGNTYSSPKRWYHFDGVWDSDSRKL-SRIYKFRGIGKA 184

Db 172 NRNVESGDYIEISAWTGFNFPPGRGDSYNSFNKWKYHFDGTDWDEGRKLNRIYKFRGIGKA 231
QY 185 WDEVDPENGNDYLMYADLMDHPPEVVTYELKKNWQKYYVNTTIDGFRDLDAVXHKIPSF 244
Db 232 WDEVSSENGNDYLMYADLMDHPPEVVTYELKKNWQKYYVNTTIDGFRDLDAVXHKIHYL 291
QY 245 FPDMLSVYRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFFYTASKSGG 304
Db 292 RDWNVHVRQOTGKMPFAVAFKNDLAAIENYLNKTSWNHVSFDPVPLHNYLNASNGN 351
QY 305 FDMRLTMTNLMKDOPTLATVFDNHDTEPGQALQSVDWDFKPLAYAFILTRQEGYPCV 364
Db 352 YDMRNLKPTGVANHPHTLAVTLVENHDSQPSQSGLESVSWFKPLAYAFILTRQEGYPSV 411
QY 365 FYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKPG 421
Db 412 FYGDYGTGKNSNYEIPALCKIDPLITARKNAYGTQHDYLDHSDIIGWTRGGSDVHAN 471
QY 422 SGLAALITDPGSGKMYGKQHAGKVFYDLTGNRSDDTVTINSDDGMBFKVNGSGSVWV 481
Db 472 SGLATLISDPGSGKMYGKQHAGKVFYDLTGNRSDDTVTINSDDGMBFKVNGSGSVIYV 531
QY 482 PR 483
Db 532 QR 533

RESULT 7
Q9RQT8 PRELIMINARY; PRT; 519 AA.
AC 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.I., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF00567.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL 1 57 POTENTIAL.
FT CHAIN 58 519 RAW STARCH DIGESTING AMYLASE.
SQ SEQUENCE 519 AA; 58337 MW; 3E6B88AA4DF98B163 CRC64;

Query Match 64.4%; Score 1837.5; DB 2; Length 519;
Best Local Similarity 67.4%; Pred. No. 1.1e-117;
Matches 326; Conservative 57; Mismatches 98; Indels 3; Gaps 1;
QY 1 AAFPNGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLPYPAYKTSRSDVGVY 60
Db 34 AAFPNGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLPYPAYKTSRSDVGVY 93
QY 61 DLYDLGEFNQKGTVRTKYGTKAQYLOAQAHAAAGQVYADVDFDHKGADGTEWDAVE 120
Db 94 DLYDLGEFNQKGTVRTKYGTKAQYLOAQAHAAAGQVYADVDFDHKGADGTEWDAVE 153
QY 121 VNPSDRNQEISCTYIOIQAWTKEFDFGRGNTYSSPKRWYHFDGVWDSDSRKL-SRIYKFRG 180
Db 154 VNPSDRNQEISCTYIOIQAWTKEFDFGRGNTYSSPKRWYHFDGVWDSDSRKL-SRIYKFRG 213

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QY 181 IGRWDEVDTEGNYDYLAMYADLMDHPVETTELKNGKMYVNTTIDGFRDLDAVKHIK 240
Db 214 TGRWDEVSSENGYDYLAMYADIDYDHPDVVNEKMGWYVANEVGLDGYRLDAVKHIK 273
QY 241 FSPFPDLVSYSRSTGKPLFTVGEYWSYDINKLHNYITKTGDTSLFADPLHNFYTASK 300
Db 274 FSLKDWVDNARAATGKEMFTVGEYQWQNDLGALNNYLAKVYNQSLFADPLHNFYAAST 333
QY 301 SGGAFTMTLNTLMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 334 GGGYDNRNLTNLVSNPFTKAVTLVENHDTQGSLESTVQWFKPLAYAFILTRSGG 393
QY 361 YPCVFGDYD---GIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGT 417
Db 394 YPSVFGDMYGTGTTTRETIPALSKIEPLLKARKDYAYGTQRDYIDNPVIGWTRREGDS 453
QY 418 EKPSGLAALITDPPGSKMYVQKQAGKVFYDITGNRSDTVTINSDGWGEFKVNGGSV 477
Db 454 TKAKSGLATVITDPPGSKMYVGTSNAGEIWTYDITGNRTDKITIGSDGYATFPVNGGSV 513
QY 478 SVWV 481
Db 514 SVWV 517

RESULT 8
Q81AS4 PRELIMINARY; PRT; 513 AA.
AC Q81AS4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Glucan 1,4-alpha-maltohexosidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AE017009; AAP10417.1;
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha.amyl_cat.
DR InterPro; IPR006589; Alp.amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BFF9FF6 CRC64;

Query Match 64.1%; Score 1829.5; DB 16; Length 513;
Best Local Similarity 65.6%; Pred. No. 3.7e-117;
Matches 315; Conservative 70; Mismatches 92; Indels 3; Gaps 1;

QY 5 NGTMQYFEWYLPDDGTLTWKVAENNLSSIGITALWLPAYKTSRSDVGYGVYDLYD 64
Db 32 NGTLMQYFEWYLPDDGTLTWKVAENNLSSIGITALWLPAYKTSRSDVGYGVYDLYD 91
QY 65 LGFEFNQKTVTKYGTAKYQALQIAQAAHAAGMQYVADVVFHKGADGTWDAVEVNP 124
Db 92 LGFEFNQKTVTKYGTAKYQALQIAQAAHAAGMQYVADVVFHKGADGTWDAVEVNP 151
QY 125 DRNQEISGTQIQAWTKFPGRGNYSFKRWTHYDFDGVWDESRKLSRIYKFRGIGA 184

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Db 152 NRNEVSGDYEISAWTGFPGRGDSYSNFKWYHFPDGTGDMDEGRKLNRIYFRGIGKA 211
QY 185 WDEVEVDTEGNYDYLAMYADLMDHPVETTELKNGKMYVNTTIDGFRDLDAVKHIKFSFF 244
Db 212 WDEVSSSENGYDYLAMYADLDFDHPDVANEMKMGWYVANEVGLDGYRLDAVKHIDHEYL 271
QY 245 PDLMSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTGDTSLFADPLHNFYTASKSGGA 304
Db 272 RDMVNHVRQQTGKEMFTVGEYQWQNDIQTLNNYLAKVYNQSLFADPLHNFYVASTGNGN 331
QY 305 FDMRTLMTLNTLMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEGYPCV 364
Db 332 YDMRNILKGVIVANHPHTLAVTLVENHDSQGSLESVSWPFKPLAYAFILTRAEGPSV 391
QY 365 FYGDIYGI---POYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRREGTEKPG 421
Db 392 FYGDIYGTGKNSYVEIPALCKIDPILTARKNFAYGTQRDYFDPDPVIGWTRREGSVHAN 451
QY 422 SGLAALITDPPGSKMYVQKQAGKVFYDITGNRSDTVTINSDGWGEFKVNGGSVWV 481
Db 452 SGLATLISDGGGAKWMDVGKNNAGEWYDITGNQNTVTITNKDQWQFQVSGSVSIYV 511

RESULT 9
Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AWS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.C., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niemman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.S., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha.amyl_cat.
DR InterPro; IPR006589; Alp.amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 64.0%; Score 1827.5; DB 16; Length 513;
Best Local Similarity 65.8%; Pred. No. 5.1e-117;
Matches 316; Conservative 69; Mismatches 92; Indels 3; Gaps 1;

QY 5 NGTMQYFEWYLPDDGTLTWKVAENNLSSIGITALWLPAYKTSRSDVGYGVYDLYD 64
Db 32 NGTLMQYFEWYLPDDGTLTWKVAENNLSSIGITALWLPAYKTSRSDVGYGVYDLYD 91
QY 65 LGFEFNQKTVTKYGTAKYQALQIAQAAHAAGMQYVADVVFHKGADGTWDAVEVNP 124

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Db 263 SDWVRHQRNEADQDLFFVVGWYKDDVGCALFYLDENWMSLFDVPLNFINFYRASQOQGS 322
Qy 305 FDMRTLTMTLMKQDPTLAVTFVNDHTEPQALQSWVDWFKPLAYAFILTRQEGYPCV 364
Db 323 YDMENILRGSVEAHFMHATVFDNHDTPQGESLESVWADFVKPLATATILTRGGYPNV 382
Qy 365 FYGDIYGIPOVNIPLSKSIDPLLIARDYAYGTQHDYLDHSDIIGWTRBGTGKPGSGL 424
Db 383 FYGDIYGIPOVNIPLSKSIDPLLIARDYAYGTQHDYLDHSDIIGWTRBGTGKPGSGL 442
Qy 425 AALITDGPQSGKMYGVCKHAGKVFYDITGNRSSTVTINSDGCEFKVKGSSVWV 481
Db 443 ATIMNSPGGSKMYGVCKHAGKVFYDITGNRSSTVTINSDGCEFKVKGSSVWV 499

RESULT 12
Q8YUZI PRELIMINARY; PRT; 492 AA.
AC Q8YUZI
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha-amylose.
GN ALR2190.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003588; BAB73889.1; -
DR FTR; AH2079; AH2079.
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylose; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KW Complete proteome.
SQ SEQUENCE 492 AA; 57063 MW; 11B5D6ECF2F18288 CRC64;

Query Match 47.1%; Score 1345.5; DB 16; Length 492;
Best Local Similarity 52.8%; Pred. No. 5e-84;
Matches 261; Conservative 67; Mismatches 147; Indels 19; Gaps 7;

Qy 2 APFNGTMMQYFEWYLPDGTGLTKVANEANLSSIGITALWLPAYKGTGRS-DVYGQVY 60
Db 2 AQWNGTMMQYFHWYIPNDGNLWSKVEASAPELADAGTAMWLPAYKGFAGSPVYGQV 61
Qy 61 DLYDLGFEQNGKVTRTKYGTQAQYLOIAQAAHAGMOMVADVDFDHKGGADGTETWDAVE 120
Db 62 DLFDLGFEQNGKVTRTKYGTQAQYLOIAQAAHAGMOMVADVDFDHKGGADGTETWDAVE 121
Qy 121 VNPESDRNQEISGTQIOAWTKFDPFGNGTYSSFKRWYHFDGVDWDB--SRKLSRIYKF 178
Db 122 FPQDRLNPKRGLQDIKTYTHNFPGRQKYSNFEWHWHFDAVDYNEYSNGDSTVYLL 181
Qy 179 RGIGKANDWEVDTEGNGYDLYMADLMDHPEVVTTELKNGKVVNTTNDIGFRLDAVKH 238
Db 182 E--GKNFDYVALEKGNFAYLMGCDLDFQNEWVGEVTVYWGKWCILDITKVDGFRIDAIK 239
Qy 239 IKFSFFDQWLSYRASQTKPLFTVGEYWSYDINKLHNYITKTDTMSLFDAPLHNKFYTA 298
Db 240 ISTWFFFEWIDALERHAGKOLFWMYGEVYNDINTLLWYVDVAVRGKMSVDFVPLHYNFQA 299
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Qy 299 SKSGAFDMRTLTMTLMKQDPTLAVTFVNDHTEPQALQSWVDWFKPLAYAFILTRQ 358
Db 300 SKSGGNYDMRILDTGTMWQRPHTAVTFVENHDSQPLQALSVVPEWFKPLAYAILLRQ 359
Qy 359 EGYPCVFGYGYGIP-----QYNI--PSLKSIDPLLIARDYAYGTQHDYLDHSD 407
Db 360 EGYPCVPHADYGYGAEYBDWKGNGRNYIFMPSHRWIIDKLLYARKHYAYGPPQNYLDHWN 419
Qy 408 IIGWTRBGTGKPGSGLAALITDGPQSGKMYGVCKHAGKVFYDITGNRSSTVTINSDGW 467
Db 420 TIGWTRLGADHDP--QGNVIMSDGSEGIKMEVGKPNP--KFIDLTEHKEAVVYNEWGW 476
Qy 468 GEFKVGSGSVWV 481
Db 477 GEFRCLGSGSVWV 490

RESULT 13
Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Alpha-amylose precursor.
GN B74690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RX Xu J., Bjurcell M.K., Himrod J., Deng S., Carmichael L.K.,
RX Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -
DR GO; GO:0004556; F:alpha-amylose activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat_sub.
DR Pfam; PF00128; alpha-amylose; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 46.3%; Score 1322.5; DB 16; Length 481;
Best Local Similarity 49.3%; Pred. No. 1.8e-82;
Matches 236; Conservative 89; Mismatches 153; Indels 1; Gaps 1;

Qy 5 NGTMMQYFEWYLPDGTGLTKVANEANLSSIGITALWLPAYKGTGRSDVYGQVYDLYD 64
Db 3 NGVMMQYFEWYLPDGTGLTKVANEANLSSIGITALWLPAYKGTGRSDVYGQVYDLYD 62
Qy 65 LGFENQKGTVRTKYGTQAQYLOIAQAAHAGMOMVADVDFDHKGGADGTETWDAVEVNS 124
Db 63 LGFEDQKGTVRTKYGTQAQYLOIAQAAHAGMOMVADVDFDHKGGADGTETWDAVEVNS 122
Qy 125 DRNQEISGTQIOAWTKFDPFGNGTYSSFKRWYHFDGVDWDBSRKLSRIYKFRGIGKA 184
Db 123 ERTKALGEPPEIQWTKYSGHGRKDKHSDFKWYHFSFGTGFDDAQKRSQVQIQSGKA 182
Qy 185 WDMEDVTENGNDYDLYMADLMDHPEVVTTELKNGKVVNTTNDIGFRLDAVKHIFKFSFF 244
Db 183 WSEGVDSNGNDYDLYMADLMDHPEVVTTELKNGKVVNTTNDIGFRLDAVKHIFKFSFF 242
Qy 245 PDMLSYVRSQTKPLFTVGEYWSYDINKLHNYITKTDTMSLFDAPLHNKFYTA 304
Db 243 AQFLDAVRSERGNDFYAVGEYWGNDLEALDAYIEAVGHKVNLFDPVPLHYNMFQASQEGKD 302
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Db	63	LGSEFNKGVTRTKYGFKEYDLOAIQALKAQGIQPMADVVLNHHKAAADHREAFQVIEVDPV	122
Qy	125	DRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDWDESRKLSRIYKFRGIGKA	184
Db	123	DRVVEGPEPTINGWTSFTFDGRQDTYNGFHHWHYFTGDTYDAKRSKSGIYLGQDNKG	182
Qy	185	WDWE--VDTENGNYDYLMYADLMDHDPVVTTELKNWGKYVNTTNIIDGFRLDAVKHKIFS	242
Db	183	WANEELVDNENGNYDYLMYADLDLPKPEVIQNIYDWDADWFMETTGAVAGFRLDAVKHDSF	242
Qy	243	FFPDWLISYRSQTGKPLFTVGEYWSYDINKLHNIITKTDTGMSLFDAPLHNKFTASKSG	302
Db	243	FMEFNFRDMKEKYGDPPYVFGFWSNDEKANLDYLEKTEEHFDLDVRLHQNLFEASQAG	302
Qy	303	GAFDMETLWNTLWKQOPTLAVTVPDNDHDTFPGQALOSWDPWPKELAYAFILIROEGYP	362
Db	303	ANYDLRGIFDLSLVELPKDCAVTPVDNHDTRQQALESVBEPFKPAAYAILIURQDGLP	362
Qy	363	CVFVGDDYVGP-QYNIPELSKSIDPLLIARRDYAYGTHDYLDHSDIIGTWREGTEKPG	421
Db	363	CVFYGYIGISGQYAAQDFEILDRLLAIRKDLAYGEQNDYFDHANCIGWRSGNENQ--	420
Qy	422	SGLAALITDPEGGSKNWYVYGQKHAGKVPFYDITGNRSPTVTINSBGWGEFKYNGGVSVMV	481
Db	421	SPIAVLISNDQENSKSMFVGEQWNTQTFVDLLGSHQGQVTTIDERGYGGFPVSARSVSVM-	479
Qy	482	PRKTTVSTI	490
Db	480	---AVNTI	484

Search completed: October 7, 2004, 00:18:57
Job time : 51.3774 secs

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 15.9573 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-6
Perfect score: 2854
Sequence: 1 AAPFNGTMMQYFEWYLPDDG.....TRPWTGCFVRWTEPRILVAMP 515

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2854	100.0	515	4	US-09-291-023A-17
2	2854	100.0	515	4	US-09-537-168-8
3	2854	100.0	515	4	US-09-540-715A-17
4	2854	100.0	549	1	US-08-720-899-6
5	2854	100.0	549	1	US-08-459-610-6
6	2854	100.0	549	2	US-08-343-804-6
7	2854	100.0	549	2	US-08-687-399-6
8	2854	100.0	549	2	US-08-600-908A-6
9	2854	100.0	549	3	US-08-683-838A-6
10	2854	100.0	549	4	US-09-636-252A-6
11	2847	99.8	514	3	US-08-182-859-6
12	2847	99.8	514	3	US-09-284-097-8
13	2847	99.8	514	4	US-09-672-459-6
14	2847	99.8	514	4	US-10-186-042-6
15	2812	98.5	515	4	US-09-381-687-7
16	2780	97.4	514	3	US-08-600-656-3
17	2780	97.4	514	3	US-09-170-670-3
18	2780	97.4	514	3	US-09-193-068-3
19	2780	97.4	514	3	US-09-183-412-3
20	2780	97.4	514	3	US-09-354-191A-3
21	2780	97.4	514	4	US-09-290-734-3
22	2780	97.4	514	4	US-09-545-586-3
23	2780	97.4	514	4	US-09-769-864-3
24	2727.5	95.6	548	1	US-08-468-700-37
25	2727.5	95.6	548	1	US-08-645-971-5
26	2727.5	95.6	548	2	US-08-468-220-35
27	2727.5	95.6	548	2	US-08-468-698-35

ALIGNMENTS

RESULT 1

US-09-291-023A-17
; Sequence 17, Application US/09291023A
; Patent No. 6309871
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Acid
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 17
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-17

Query Match 100.0%; Score 2854; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. NO. 5.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLGLITALLWLPAYKGTSRSDVGGVY	60
Db	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLGLITALLWLPAYKGTSRSDVGGVY	60
Qy	61	DLVDLGEFNGKGTVRTKYGTAQYLOAIQAHAAGMOVYADVVDHKGADGTEWDAVE	120
Db	61	DLVDLGEFNGKGTVRTKYGTAQYLOAIQAHAAGMOVYADVVDHKGADGTEWDAVE	120
Qy	121	VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Db	121	VNPSDRNQEISGTYQIQAWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Qy	181	IGKAWDEWTEGNGYDLYMAYDLMDHPVVTTELKNGKWYVNTTINDGFRDLDAVKHK	240
Db	181	IGKAWDEWTEGNGYDLYMAYDLMDHPVVTTELKNGKWYVNTTINDGFRDLDAVKHK	240
Qy	241	FSEPPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDTGMSLFDAPLHNKFYASK	300
Db	241	FSEPPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDTGMSLFDAPLHNKFYASK	300
Qy	301	SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDWDFKFLAYAFILTRQEG	360

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Db 301 SGGAFDMRTLMTNTLMDKQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Qy 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Qy 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Qy 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515

RESULT 2
US-09-537-168-8
; Sequence 8, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Franzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-537-168-8

Query Match 100.0%; Score 2854; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 5.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSLGITLMLPPAYKGTSRSDVGYY 60
Db 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSLGITLMLPPAYKGTSRSDVGYY 60
Qy 61 DLYDLGEFNQKGTVRTKYGKQYLOAIQAAHAAGMOVYADVVDHKGADGTEWDAVE 120
Db 61 DLYDLGEFNQKGTVRTKYGKQYLOAIQAAHAAGMOVYADVVDHKGADGTEWDAVE 120
Qy 121 VNPSDRNQEISGTYYQIQAQWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Db 121 VNPSDRNQEISGTYYQIQAQWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Qy 181 IGKAWDEVDTEGNYDYLMDHDPHVVTELKNWGWYVNTNIDGFRDLDAVKHLK 240
Db 181 IGKAWDEVDTEGNYDYLMDHDPHVVTELKNWGWYVNTNIDGFRDLDAVKHLK 240
Qy 241 PSFPDMLSVRSQTKPLFTVGEYWSYDINKLHNYITKDTGMSLFDAPLHNKFTASK 300
Db 241 PSFPDMLSVRSQTKPLFTVGEYWSYDINKLHNYITKDTGMSLFDAPLHNKFTASK 300
Qy 301 SGGAFDMRTLMTNTLMDKQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 301 SGGAFDMRTLMTNTLMDKQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Qy 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Qy 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Qy 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
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Qy 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Qy 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515

RESULT 3
US-09-540-715A-17
; Sequence 17, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Acids
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Bacillus
US-09-540-715A-17

Query Match 100.0%; Score 2854; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 5.4e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSLGITLMLPPAYKGTSRSDVGYY 60
Db 1 AAPFNGTMMQYFEWYLPDDGTLTKVANEANNLSSLGITLMLPPAYKGTSRSDVGYY 60
Qy 61 DLYDLGEFNQKGTVRTKYGKQYLOAIQAAHAAGMOVYADVVDHKGADGTEWDAVE 120
Db 61 DLYDLGEFNQKGTVRTKYGKQYLOAIQAAHAAGMOVYADVVDHKGADGTEWDAVE 120
Qy 121 VNPSDRNQEISGTYYQIQAQWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Db 121 VNPSDRNQEISGTYYQIQAQWTKFDPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Qy 181 IGKAWDEVDTEGNYDYLMDHDPHVVTELKNWGWYVNTNIDGFRDLDAVKHLK 240
Db 181 IGKAWDEVDTEGNYDYLMDHDPHVVTELKNWGWYVNTNIDGFRDLDAVKHLK 240
Qy 241 PSFPDMLSVRSQTKPLFTVGEYWSYDINKLHNYITKDTGMSLFDAPLHNKFTASK 300
Db 241 PSFPDMLSVRSQTKPLFTVGEYWSYDINKLHNYITKDTGMSLFDAPLHNKFTASK 300
Qy 301 SGGAFDMRTLMTNTLMDKQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 301 SGGAFDMRTLMTNTLMDKQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Qy 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Qy 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Db 421 GSGLAALITDGPGGSKMWYVGKQHAGKVFYDLTGNRSDTVTINS DGMGEFKVNGGSVSW 480
Qy 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP 515
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Db 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515

RESULT 4

US-08-720-899-6

; Sequence 6, Application US/08720899

; Patent No. 5753460

; GENERAL INFORMATION:

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Borchert, Torben Vedel

; APPLICANT: Svendsen, Allan

; APPLICANT: Thellersen, Marianne

; APPLICANT: Van der Zee, Pia

; TITLE OF INVENTION: AMYLASE VARIANTS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5753460 No. 5753460disk of No. 5753460th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,899

; FILING DATE: 10-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/343,804

; FILING DATE: 22-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney Dr., Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4054.214-US

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 549 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-720-899-6

Query Match 100.0%; Score 2854; DB 1; Length 549;

Best Local Similarity 100.0%; Pred. No. 6e-246;

Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPFGTMMQYFEWYLPDDGTLTKVANEANLSSGLITALLWLPAYKGTSRSDVGXGY 60

Db 35 AAPFGTMMQYFEWYLPDDGTLTKVANEANLSSGLITALLWLPAYKGTSRSDVGXGY 94

Qy 61 DLYDLGSEFNOKGTVRTKYTKAQYLQIAAHAAGMOMYADVDFVDFHKGADGTWVDV 120

Db 95 DLYDLGSEFNOKGTVRTKYTKAQYLQIAAHAAGMOMYADVDFVDFHKGADGTWVDV 154

Qy 121 VNPDSRNOEISGTYQIQAWTKFDPGRGNTVSSFKRWYHFDGVDWDESRKLSRIYKFRG 180

Db 155 VNPDSRNOEISGTYQIQAWTKFDPGRGNTVSSFKRWYHFDGVDWDESRKLSRIYKFRG 214

Qy 181 IGRKAWDEVDTENGNYDYLMDPEVVTBELKXWGWYVNTNIDGFRDLDAVKHIK 240

Db 215 IGRKAWDEVDTENGNYDYLMDPEVVTBELKXWGWYVNTNIDGFRDLDAVKHIK 274

Qy 241 FSPFPDWLSYRSQTGKPLFTVGYWSYDINKLHNYITKTGTSLSLFDAPLHNKFTASK 300

Db 275 FSPFPDWLSYRSQTGKPLFTVGYWSYDINKLHNYITKTGTSLSLFDAPLHNKFTASK 334

Qy 301 SGGAFDMRTLTMTNTLMKQDPTLATVFDVNDHDTGEGALQSQWDPWFKPLAYAFILTRQEG 360

Db 335 SGGAFDMRTLTMTNTLMKQDPTLATVFDVNDHDTGEGALQSQWDPWFKPLAYAFILTRQEG 394

Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYVAGTQHDYLDHSDIIGWTRREGGTEKP 420

Db 395 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYVAGTQHDYLDHSDIIGWTRREGGTEKP 454

Qy 421 GSGLAALITDGPCKGSKMYGKQHAGKVFDYDLTGNSRSDTVTINSDDGWGEFKVNGSGSVW 480

Db 455 GSGLAALITDGPCKGSKMYGKQHAGKVFDYDLTGNSRSDTVTINSDDGWGEFKVNGSGSVW 514

Qy 481 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 515

Db 515 VPRKTTVSTIARPIITRPWTGEFVRWTEPRLVAMP 549

RESULT 5

US-08-459-610-6

; Sequence 6, Application US/08459610

; Patent No. 5801043

; GENERAL INFORMATION:

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Borchert, Torben Vedel

; APPLICANT: Svendsen, Allan

; APPLICANT: Thellersen, Marianne

; APPLICANT: Van der Zee, Pia

; TITLE OF INVENTION: AMYLASE VARIANTS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5801043 No. 5801043disk of No. 5801043th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,610

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/343,804

; FILING DATE: 22-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney Dr., Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4054.214-US

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 549 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-459-610-6

Query Match 100.0%; Score 2854; DB 1; Length 549;

Best Local Similarity 100.0%; Pred. No. 6e-246;

Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPFGTMMQYFEWYLPDDGTLTKVANEANLSSGLITALLWLPAYKGTSRSDVGXGY 60

Db 35 AAPFGTMMQYFEWYLPDDGTLTKVANEANLSSGLITALLWLPAYKGTSRSDVGXGY 94

Qy 61 DLYDLGSEFNOKGTVRTKYTKAQYLQIAAHAAGMOMYADVDFVDFHKGADGTWVDV 120

Db 95 DLYDLGEBFNQKGVTRTKYGTGAQYLQAIQAHAAGMQVYADVDFDHKGADGTEWDAVE 154
Qy 121 VNPSSDRNQEISGTYQIOAWTKFDPGGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Db 155 VNPSSDRNQEISGTYQIOAWTKFDPGGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214
Qy 181 IGKAWDEVDTEGNTYDYLMDHDEPVTTELKNGKQWYNTTNDGFRDLDAVKHIK 240
Db 215 IGKAWDEVDTEGNTYDYLMDHDEPVTTELKNGKQWYNTTNDGFRDLDAVKHIK 274
Qy 241 FSPFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTDGTMSPDAPLHNKFTASK 300
Db 275 FSPFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTDGTMSPDAPLHNKFTASK 334
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Db 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 420
Db 395 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 454
Qy 421 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNSRSDTVTINSDCGWGEPKVGSGSVW 480
Db 455 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNSRSDTVTINSDCGWGEPKVGSGSVW 514
Qy 481 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 549

RESULT 6
US-08-343-804-6
; Sequence 6, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,804
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 549 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-804-6

Query Match 100.0%; Score 2854; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 6e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAFPNGTMMQYFEWYLPDDGTLMTKVNANANLSSIGITALLWLPAYKGTSRSDVGYG 60
Db 35 AAFPNGTMMQYFEWYLPDDGTLMTKVNANANLSSIGITALLWLPAYKGTSRSDVGYG 94
Qy 61 DLYDLGEBFNQKGVTRTKYGTGAQYLQAIQAHAAGMQVYADVDFDHKGADGTEWDAVE 120
Db 95 DLYDLGEBFNQKGVTRTKYGTGAQYLQAIQAHAAGMQVYADVDFDHKGADGTEWDAVE 154
Qy 121 VNPSSDRNQEISGTYQIOAWTKFDPGGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Db 155 VNPSSDRNQEISGTYQIOAWTKFDPGGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 214
Qy 181 IGKAWDEVDTEGNTYDYLMDHDEPVTTELKNGKQWYNTTNDGFRDLDAVKHIK 240
Db 215 IGKAWDEVDTEGNTYDYLMDHDEPVTTELKNGKQWYNTTNDGFRDLDAVKHIK 274
Qy 241 FSPFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTDGTMSPDAPLHNKFTASK 300
Db 275 FSPFPDWLSYVRSGTKPLFTVGEYWSYDINKLHNYITKTDGTMSPDAPLHNKFTASK 334
Qy 301 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 360
Db 335 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG 394
Qy 361 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 420
Db 395 YPCVFYGDYGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTRGGTEKP 454
Qy 421 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNSRSDTVTINSDCGWGEPKVGSGSVW 480
Db 455 GSGLAALITDGPCKGSKWYVKGQHAGKVFDYDLTGNSRSDTVTINSDCGWGEPKVGSGSVW 514
Qy 481 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 515
Db 515 VPRKTTVSTIARPIITRPWTGFEVRWTEPRLVAMP 549

RESULT 7
US-08-687-399-6
; Sequence 6, Application US/08687399
; Patent No. 5928381
; GENERAL INFORMATION:
; APPLICANT: Toft, Annette H.
; APPLICANT: Marcher, Dorte
; APPLICANT: Pedersen, Hanne H.
; APPLICANT: Nilsson, Thomas E.
; TITLE OF INVENTION: A Combined Desizing and Bleaching
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5928381o No. 5928381disk of No. 5928381th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,399
; FILING DATE:
; CLASSIFICATION: 008
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4127.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 549 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-687-399-6

Query Match 100.0%; Score 2854; DB 2; Length 549;
 Best Local Similarity 100.0%; Pred. No. 6e-246;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLIGITALWLPAYKGTSRSDVG	60
DB	35	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLIGITALWLPAYKGTSRSDVG	94
QY	61	DLVDLGEFNGKGTVRTKYGTAKQYLOAIQAAHAAGMOMVADVDFDHKGADGT	120
DB	95	DLVDLGEFNGKGTVRTKYGTAKQYLOAIQAAHAAGMOMVADVDFDHKGADGT	154
QY	121	VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDMDESKLSRIYK	180
DB	155	VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDMDESKLSRIYK	214
QY	181	IGKAWDEVDTEGNDYDLYMYADLDMDHPEVTVTELKNWGWYNTTINIDGFR	240
DB	215	IGKAWDEVDTEGNDYDLYMYADLDMDHPEVTVTELKNWGWYNTTINIDGFR	274
QY	241	FSFPDWLSVRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNK	300
DB	275	FSFPDWLSVRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNK	334
QY	301	SGGAFDMRTLTMTNLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAY	360
DB	335	SGGAFDMRTLTMTNLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAY	394
QY	361	YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIIG	420
DB	395	YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIIG	454
QY	421	GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDGWGEFK	480
DB	455	GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDGWGEFK	514
QY	481	VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP	515
DB	515	VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP	549

RESULT 8
 US-08-600-908A-6
 ; Sequence 6, Application US/08600908A
 ; Patent No. 5989169
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Big rd-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: "-Amylase Mutants
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/600,908A
 ; FILING DATE: 13-FEB-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Green, Reza
 ; REGISTRATION NUMBER: 38,475
 ; REFERENCE/DOCKET NUMBER: 4394.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 549 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-600-908A-6

Query Match 100.0%; Score 2854; DB 2; Length 549;
 Best Local Similarity 100.0%; Pred. No. 6e-246;
 Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLIGITALWLPAYKGTSRSDVG	60
DB	35	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNSLIGITALWLPAYKGTSRSDVG	94
QY	61	DLVDLGEFNGKGTVRTKYGTAKQYLOAIQAAHAAGMOMVADVDFDHKGADGT	120
DB	95	DLVDLGEFNGKGTVRTKYGTAKQYLOAIQAAHAAGMOMVADVDFDHKGADGT	154
QY	121	VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDMDESKLSRIYK	180
DB	155	VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDMDESKLSRIYK	214
QY	181	IGKAWDEVDTEGNDYDLYMYADLDMDHPEVTVTELKNWGWYNTTINIDGFR	240
DB	215	IGKAWDEVDTEGNDYDLYMYADLDMDHPEVTVTELKNWGWYNTTINIDGFR	274
QY	241	FSFPDWLSVRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNK	300
DB	275	FSFPDWLSVRSOTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDPALHNK	334
QY	301	SGGAFDMRTLTMTNLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAY	360
DB	335	SGGAFDMRTLTMTNLTKMDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAY	394
QY	361	YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIIG	420
DB	395	YPCVFYGDYIGIPOYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIIG	454
QY	421	GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDGWGEFK	480
DB	455	GSGLAALITDGPCKGKMYVKGQHAGKVFYDLTGNSRSDTVTINSDGWGEFK	514
QY	481	VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP	515
DB	515	VPRKTTVSTIARPIITTRPWTGFEFVRWTEPRLVAMP	549

RESULT 9
 US-08-683-838A-6
 ; Sequence 6, Application US/08683838A
 ; Patent No. 6022724
 ; GENERAL INFORMATION:
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Big rd-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; TITLE OF INVENTION: "-Amylase Mutants
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:

ADDRESS: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,838A
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-838A-6

Query Match 100.0%; Score 2854; DB 3; Length 549;
Best Local Similarity 100.0%; Pred. No. 6e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALTALWLPAYKGTSRSDVG	60
DB	35	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALTALWLPAYKGTSRSDVG	94
QY	61	DLYDLGEFNGKGTVRTKYGTAKYQALQIAAHAAGMQVYADVDFDHKGADGTEWDAVE	120
DB	95	DLYDLGEFNGKGTVRTKYGTAKYQALQIAAHAAGMQVYADVDFDHKGADGTEWDAVE	154
QY	121	VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
DB	155	VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	214
QY	181	IGKAWDEVDTEGNYDYLMDHDPVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	240
DB	215	IGKAWDEVDTEGNYDYLMDHDPVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	274
QY	241	FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK	300
DB	275	FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK	334
QY	301	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDWPFKPLAYAFILTRQEG	360
DB	335	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDWPFKPLAYAFILTRQEG	394
QY	361	YPCVFYGDYGIPOYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	420
DB	395	YPCVFYGDYGIPOYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	454
QY	421	GSGLAALITDGPCKGKMYVKGQHAGKVFDLTGNRSDDVTINSDCGWGPKVNGGSSVSW	480
DB	455	GSGLAALITDGPCKGKMYVKGQHAGKVFDLTGNRSDDVTINSDCGWGPKVNGGSSVSW	514
QY	481	VPRKTTVSTIARPIITPRPWTGEFVRWTEPRLVAMP	515
DB	515	VPRKTTVSTIARPIITPRPWTGEFVRWTEPRLVAMP	549

RESULT 11
US-09-182-859-6
Sequence 6, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants

RESULT 10
US-09-636-252A-6
Sequence 6, Application US/09636252A
Patent No. 6440716
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
TYPE: PRT
LENGTH: 549
ORGANISM: B. stearothermophilus
US-09-636-252A-6

Query Match 100.0%; Score 2854; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 6e-246;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALTALWLPAYKGTSRSDVG	60
DB	35	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALTALWLPAYKGTSRSDVG	94
QY	61	DLYDLGEFNGKGTVRTKYGTAKYQALQIAAHAAGMQVYADVDFDHKGADGTEWDAVE	120
DB	95	DLYDLGEFNGKGTVRTKYGTAKYQALQIAAHAAGMQVYADVDFDHKGADGTEWDAVE	154
QY	121	VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
DB	155	VNPSDRNQEISGTYQIQAWTKFDPGKNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	214
QY	181	IGKAWDEVDTEGNYDYLMDHDPVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	240
DB	215	IGKAWDEVDTEGNYDYLMDHDPVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	274
QY	241	FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK	300
DB	275	FSFPFOWLSVRSQTKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTYASK	334
QY	301	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDWPFKPLAYAFILTRQEG	360
DB	335	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDWPFKPLAYAFILTRQEG	394
QY	361	YPCVFYGDYGIPOYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	420
DB	395	YPCVFYGDYGIPOYNIPLSKSIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	454
QY	421	GSGLAALITDGPCKGKMYVKGQHAGKVFDLTGNRSDDVTINSDCGWGPKVNGGSSVSW	480
DB	455	GSGLAALITDGPCKGKMYVKGQHAGKVFDLTGNRSDDVTINSDCGWGPKVNGGSSVSW	514
QY	481	VPRKTTVSTIARPIITPRPWTGEFVRWTEPRLVAMP	515
DB	515	VPRKTTVSTIARPIITPRPWTGEFVRWTEPRLVAMP	549

FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182.859
EARLIER FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0712/96
EARLIER FILING DATE: 1996-06-28
EARLIER APPLICATION NUMBER: 0775/96
EARLIER FILING DATE: 1996-07-11
EARLIER APPLICATION NUMBER: 1263/96
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-182-859-6

Query Match 99.8%; Score 2847; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITATLWLPAYKTSRSDVGYVY	60
Db	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITATLWLPAYKTSRSDVGYVY	60
Qy	61	DLVDLGEFNQKGTVRTKYGTAKQYLQAIQAHAAGMOVYADVVDHKGADGTEWDAVE	120
Db	61	DLVDLGEFNQKGTVRTKYGTAKQYLQAIQAHAAGMOVYADVVDHKGADGTEWDAVE	120
Qy	121	VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Db	121	VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Qy	181	IGKAWDEVDTEGNDYLYADLMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	240
Db	181	IGKAWDEVDTEGNDYLYADLMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	240
Qy	241	FSFPDMLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK	300
Db	241	FSFPDMLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK	300
Qy	301	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG	360
Db	301	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG	360
Qy	361	YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	420
Db	361	YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	420
Qy	421	GSGLAALITDGPCKGSKMYVKGQHAGKVYFDLTGNRSDDTVTINSDGWGEFKVNGGSVSW	480
Db	421	GSGLAALITDGPCKGSKMYVKGQHAGKVYFDLTGNRSDDTVTINSDGWGEFKVNGGSVSW	480
Qy	481	VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV	514
Db	481	VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV	514

RESULT 12
US-09-264-097-8
Sequence 8, Application US/09264097
Patent No. 6287826
GENERAL INFORMATION:
APPLICANT: Hendriksen, Hanne Vang
APPLICANT: No. 6287826man, Barrie Edmund
TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264.097
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98

EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus
US-09-264-097-8

Query Match 99.8%; Score 2847; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITATLWLPAYKTSRSDVGYVY	60
Db	1	AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITATLWLPAYKTSRSDVGYVY	60
Qy	61	DLVDLGEFNQKGTVRTKYGTAKQYLQAIQAHAAGMOVYADVVDHKGADGTEWDAVE	120
Db	61	DLVDLGEFNQKGTVRTKYGTAKQYLQAIQAHAAGMOVYADVVDHKGADGTEWDAVE	120
Qy	121	VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Db	121	VNPSDRNOEISGTYQIQAWTKFDPGCGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG	180
Qy	181	IGKAWDEVDTEGNDYLYADLMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	240
Db	181	IGKAWDEVDTEGNDYLYADLMDHPEVVTTELKNGKMYVNTNIDGFRDLDAVKHIK	240
Qy	241	FSFPDMLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK	300
Db	241	FSFPDMLSVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGMSLFDAPLHNKFTYASK	300
Qy	301	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG	360
Db	301	SGGAFDMRTLMTNLMKDQPTLAVTFVDNHDTEPGQALQSWDPWFKPLAYAFILTRQEG	360
Qy	361	YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	420
Db	361	YPCVFYGDYIGIPQYNIPSLKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP	420
Qy	421	GSGLAALITDGPCKGSKMYVKGQHAGKVYFDLTGNRSDDTVTINSDGWGEFKVNGGSVSW	480
Db	421	GSGLAALITDGPCKGSKMYVKGQHAGKVYFDLTGNRSDDTVTINSDGWGEFKVNGGSVSW	480
Qy	481	VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV	514
Db	481	VPRKTTVSTIARPTTRPWTGFEFVRWTEPRLVAV	514

RESULT 13
US-09-672-459-6
Sequence 6, Application US/09672459
Patent No. 6436888
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/672.459
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/182,859
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 0515/96
PRIOR FILING DATE: 1996-04-30
PRIOR APPLICATION NUMBER: 0712/96
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: 0775/96
PRIOR FILING DATE: 1996-07-11
PRIOR APPLICATION NUMBER: 1263/96

; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 514
; TYPE: PR1
; ORGANISM: Bacillus stearothermophilus
US-09-672-459-6

Query Match 99.8%; Score 2847; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-245;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAPNGTMMQYFEWYLPDDGTLTKVANEANNLSSGITALWLPAYKGTSRSDVGYY 60
Db 1 AAPNGTMMQYFEWYLPDDGTLTKVANEANNLSSGITALWLPAYKGTSRSDVGYY 60

Qy 61 DLYDLGEFNQKGTVRTKYGTAKYQALQIAAHAAGMQYADVVDHKGADGTWDAVE 120
Db 61 DLYDLGEFNQKGTVRTKYGTAKYQALQIAAHAAGMQYADVVDHKGADGTWDAVE 120

Qy 121 VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Db 121 VNPSDRNQEISGTYQIQAWTKFDPGGRNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180

Qy 181 IGKAWDEVDTEGNYDYLAMYADLMDHPVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240
Db 181 IGKAWDEVDTEGNYDYLAMYADLMDHPVVTTELKNWGWYVNTTNDGFRDLDAVKHIK 240

Qy 241 FSFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300
Db 241 FSFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHNKFTASK 300

Qy 301 SGGAFDMRTLMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360
Db 301 SGGAFDMRTLMTNTLMKQDPTLAVTFVDNHDTEPGQALQSWDPWPKPLAYAFILTRQEG 360

Qy 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420
Db 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGGTEKP 420

Qy 421 GSGLAALITDGPQSGKMWYVKGQHAGKVFDLTGNRSDTVTINSOGWGEFKVNGGSVSW 480
Db 421 GSGLAALITDGPQSGKMWYVKGQHAGKVFDLTGNRSDTVTINSOGWGEFKVNGGSVSW 480

Qy 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRVAV 514
Db 481 VPRKTTVSTIARPIITRPWTGFEVFWTEPRVAV 514

RESULT 14

US-10-186-042-6
; Sequence 6, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186, 042
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672, 459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182, 859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96

RESULT 15

US-09-381-687-7
; Sequence 7, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
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; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 515
; TYPE: PR1
; ORGANISM: B. stearothermophilus

US-09-381-687-7

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Query Match      98.5%; Score 2812; DB 4; Length 515;
Best Local Similarity 98.8%; Pred. No. 3e-242;
Matches 509; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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